

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 15:03:38 ; Search time 8754 seconds  
(without alignments)  
11236.473 Million cell updates/sec

Title: US-10-643-676-1  
Perfect score: 2030  
Sequence: 1 cttcctagaagatggacca.....ttagattacaacacaaaag 2030

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 2422767955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2030	100.0	2030	6	AX548023 Sequence
2	2030	100.0	2042	6	AX548024 Sequence
3	2030	100.0	111945	8	AL022224 Arabidops
4	2030	100.0	198427	8	AL161552 Arabidops
5	1064	52.4	1064	6	AX509457 Sequence
6	211.8	10.4	288	11	AL807890 Arabidops
7	211.8	10.4	290	11	BX295033 Arabidops
8	95.4	4.7	1001	8	AY086004 Arabidops
9	93	4.6	348174	3	CR382399 Plasmodiu
10	91.2	4.5	135203	9	AC025278 Homo sapi
11	90.2	4.4	8056	6	AX599046 Sequence
12	89.4	4.4	104992	2	AC005504 Plasmodiu
13	89.4	4.4	169546	2	AC004157 Plasmodiu
14	89.4	4.4	250421	2	AE014849 Plasmodiu
15	89.2	4.4	26565	2	AC119399 Homo sapi
16	88.4	4.4	115218	9	HS159A1 Human DNA
17	88.4	4.4	136240	3	AC117070 Dictyoste
18	87	4.3	195319	2	CR388410 Danio rer
19	86.8	4.3	1496	3	CEY53C12D Caenorhab

C	20	86.6	4.3	167592	2	CR847845	CR847845	Danio rer
C	21	86.4	4.3	223509	2	CR388007	CR388007	Danio rer
	22	85.8	4.2	160645	2	CR391949	CR391949	Danio rer
	23	85.8	4.2	236582	2	CR388102	CR388102	Danio rer
	24	85.6	4.2	110000	2	CR555291_2	Continuation (3 of	
	25	85	4.2	191707	2	CR847971	CR847971	Danio rer
	26	84.8	4.2	175544	2	AC117342	AC117342	Rattus no
	27	84.6	4.2	185048	2	CR392021	CR392021	Danio rer
C	28	84.4	4.2	143685	2	CR450770	CR450770	Danio rer
	29	84.4	4.2	180861	2	CR391970	CR391970	Danio rer
C	30	84.4	4.2	190482	2	CR450828	CR450828	Danio rer
	31	84.4	4.2	302156	3	AC116977	AC116977	Dictyoste
	32	84.2	4.1	57538	3	AC115882	AC115882	Dictyoste
	33	84.2	4.1	257757	3	AE014837	AE014837	Plasmodiu
	34	84	4.1	110000	3	AE016957_0	AE016957	Dictyoste
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C	36	84	4.1	233658	2	CR354421	CR354421	Danio rer
C	37	84	4.1	250663	3	AE014826	AE014826	Plasmodiu
C	38	83.8	4.1	1070	8	AY093084	AY093084	Arabidops
C	39	83.8	4.1	75076	9	AC004948	AC004948	Homo sapi
C	40	83.8	4.1	183584	9	AC012492	AC012492	Homo sapi
C	41	83.8	4.1	202863	2	BX927344	BX927344	Danio rer
C	42	83.4	4.1	192187	3	AC117072	AC117072	Dictyoste
C	43	83	4.1	105238	9	AC011458	AC011458	Homo sapi
C	44	83	4.1	251762	3	AE014851	AE014851	Plasmodiu
C	45	83	4.1	347582	3	PFMAL4P1	AL034557	Plasmodiu

ALIGNMENTS

RESULT 1  
AX548023 2030 bp DNA linear PAT 26-NOV-2002  
LOCUS Sequence 1 from Patent WO02068665.  
DEFINITION AX548023  
ACCESSION AX548023  
VERSION AX548023.1 GI:25813131  
KEYWORDS Arabidopsis thaliana (thale cress)  
SOURCE Arabidopsis thaliana  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1  
AUTHORS Thomas, T., Nuccio, M. and Hsieh, T.F.  
TITLE Constitutive promoter from arabidopsis  
JOURNAL Patent: WO 02068665-A 1 06-SEP-2002;  
Rhubio (FR)

FEATURES  
source Location/Qualifiers  
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/organism="Arabidopsis thaliana"  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e-292;  
Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 61 AAATCATATTCATTACAAAAGGAAAAAATAATTTTCTATCTCTAAGTTAATAC 120  
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DB 181 TTTTAGAAAAATGTATCTTTTCATATATAAAATATATAGATCTTCAAGAACTGAAT 240

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241	Qy	GGGTTTTCAACTATTTTTATCGTTTGCACACTCTTTGACTTATCAAAAAGAGTTTCAAAATA	300
241	Db		
241	Db	GGGTTTTCAACTATTTTTATCGTTTGCACACTCTTTGACTTATCAAAAAGAGTTTCAAAATA	300
301	Qy	GA AAAATAGAAATCGAAATCACA CGTTTGCAGTGTAGAGGGATTTGATATTTGGTTCGACATTT	360
301	Db	GA AAAATAGAAATCGAAATCACA CGTTTGCAGTGTAGAGGGATTTGATATTTGGTTCGACATTT	360
361	Qy	TAAAGAGTTGTTTGTTTTTTTTTTTTCCAAATCTGCAATCGTTTTCGTTCCGTTTGACCAAAAT	420
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421	Qy	TCAACACTTTGTATATAAACCAGAAATAGTATAATCTAGACGTACGCCAATACCAAAAATAAAA	480
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481	Qy	ATTA AAAACTCAATTCACAAATTTGAATCTTACACCAATATCATGCAATATATATCAGCAACTTA	540
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721	Db	TATGTTTAACTACAGATCACCATCCACAATTAACAATCCGATTTGGTGGCGGCCATTTGTT	780
781	Qy	TCGATATTTGCGCAACTGTGATTTGATGTGACTGCCAGCTGGCATATTTTCCCTCCTCATTT	840
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901	Db	GTCTTTTCACTTTTAAAGAAAACCCAAACCGGAAATCAACTATACGAAATCACAATGT	960
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1021	Db	GTGCTTAAACCGAAAAACAGAAAACGGTTTATGACGCCAACGAGGCAAGAGGGGTAAAAACGAA	1080
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Db	1321	TC	TCGTTTCGATTC	AGATACG	ATTTTTCG	ATGTTTCAT	GTGAATG	AACCTCTG	TTTTATTAC	1380	
Qy	1381	TACT	AGGGTGTTC	CAATAT	TTTTTCCG	AGAAAT	TACCAG	AGGAA	CAAAAGTTAGTG	ATAT	1440
Db	1381	TACT	AGGGTGTTC	CAATAT	TTTTTCCG	AGAAAT	TACCAG	AGGAA	CAAAAGTTAGTG	ATAT	1440
Qy	1441	TG	ATGCAG	AGTATGA	AGTAAT	TATATAC	ATAAAT	CATGTTTGT	CTCAAG	CACTACGT	1500
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Qy	1561	ATA	ATAGTGA	ACCACTCT	CTTTTC	ATAC	ACCA	AAAAA	AAAAATTTG	AAAAAAT	1620
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Qy	1681	AT	TTTTTGG	CATGG	CAATAT	TGTC	GCAG	TAAAT	TATAC	CAATAG	1740
Db	1681	AT	TTTTTGG	CATGG	CAATAT	TGTC	GCAG	TAAAT	TATAC	CAATAG	1740
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Qy	1921	TT	TTTTCGT	ATATTC	TTCTTTG	TGTA	AAAA	TAAAT	TATG	TGTTAT	1980
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AX548024											
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AX548024											
DEFINITION											
Sequence 2 from Patent WO20068665.											
ACCESSION											
AX548024											
VERSION											
AX548024.1											
KEYWORDS											
GI:25813132											
SOURCE											
Arabidopsis thaliana (thale cress)											
ORGANISM											
Arabidopsis thaliana											
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi											
1											
REFERENCE											
Thomas, T., Nuccio, M. and Hsieh, T. F.											
Constitutive promoter from arabidopsis											
Patent: WO 02068665-A 2 06-SEP-2002;											
Rhubio											
(FR)											
Location/Qualifiers											
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ORIGIN											

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Db	1807	CTGTTCTTGCTTTTTCGTTTATAGAACATTTGAATATGATCTTTTGTGTTTTCACCC	1866
Qy	1861	AGTAGATATGATATACACATAGTAAGTAACATGGTAGTTTATATATAGAGAGATTGA	1920
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Qy	1981	GACAGATTGTTTCAGCTGAGAAAGTTTAAATTTAGATTAAACACAAAAAG	2030
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RESULT 3

ATP1C12

LOCUS

DEFINITION

Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (BSSA

ATP1C12

111945 bp

DNA

linear

PLN 20-SEP-1999

project).	intron	16955. .17005
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		17765. .17840
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and 5 can be viewed at: <a href="http://www.mips.biochem.mpg.de/proj/thal/">http://www.mips.biochem.mpg.de/proj/thal/</a> .	exon	/product="putative protein"
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REFERENCE	1		
AUTHORS	Harper, J.F., Kreps, J., Wang, X. and Zhu, T.		
TITLE	Stress-regulated genes of plants, transgenic plants containing same, and methods of use		
JOURNAL	Patent: WO 0216655-A 4152 28-FEB-2002;		
	The Scripps Research Institute (US) ; Syngenta Participations AG (CH)		
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 REFERENCE  
 1 Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Murphy, G., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M.

JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 288)  
 AUTHORS Clarke, J.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-JUL-2002) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK  
 COMMENT AT denotes an activation tag dissociation transposon within a single line, Et an enhancer trap dissociation transposon, Gr a gene trap dissociation transposon, Mt a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. \_3 denotes a sequence derived from the 3' end of the transposon, \_5 denotes a sequence derived from the 5' end of the transposon. BBSRC GARNET, ATIS project  
 On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock code: N109915.  
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 QY 215 GTTCCATTAATTCAGAGAGACAAATTAATCAGTTTCGTGTGTTTGGAGAGAGAAACA 156  
 Db |||  
 QY 1221 GATCAATACGAGAGAGATCTCTAAAGAGATTTATCGTTTCAAGTAGTCTTTATCA 1280  
 Db |||  
 QY 155 GATCAATACGAGAGAGATCTCTAAAGAGATTTATCGTTTCAAGTAGTCTTTATCA 96  
 Db |||  
 QY 1281 AACTCTTAATTAACAATCAAAACATGAACACGTGCTGTTCTCGTTTCGATTTCTAGAT 1340  
 Db |||  
 QY 95 AACTCTTAATTAACAATCAAAACATGAACACGTGCTGTTCTCGTTTCGATTTCTAGAT 36  
 Db |||  
 QY 1341 ACGATTTTATGTTTCATGTAATGAACCTCTGTTT 1375  
 Db |||  
 QY 35 ACGATTTTATGTTTCATGTAATGAACCTCTGTTT 1  
 Db |||  
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 BX295033/c 290 bp DNA linear STS 11-JUN-2003  
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 DEFINITION  
 ACCESSION BX295033  
 VERSION BX295033.1 GI:29149723  
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 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 REFERENCE  
 1 Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Murphy, G., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M.  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 290)  
 AUTHORS Clarke, J.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-MAR-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK  
 COMMENT AT denotes an activation tag dissociation transposon within a single line, Et an enhancer trap dissociation transposon, Gr a gene trap dissociation transposon, Mt a mis-expression enhancer trap

dissociation transposon, SM a defective suppressor mutator transposon. \_3 denotes a sequence derived from the 3'-end of the transposon, \_5 denotes a sequence derived from the 5'-end of the transposon. BBSRC GARNET, ATIS project  
On-line seed stock requests: <http://nasc.nott.ac.uk/NASC/stockcode/N120195>.

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Matches 213; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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ACCESSION
AY086004.1 GI:21404714
VERSION
FLI CDNA.
KEYWORDS
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
1 (bases 1 to 1001)
Haas,B.J., Volkovsky,N., Town,C.D., Troughan,M., Alexandrov,N.,
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
JOURNAL
Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE
22088475
PUBMED
12093376
REFERENCE
2 (bases 1 to 1001)
Brover,V., Troughan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Full-length cDNA from Arabidopsis thaliana
Unpublished
3 (bases 1 to 1001)
Brover,V., Troughan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Direct Submission
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of
this set was done by comparison with known proteins: two percent of

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the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genet carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

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Query Match      4.7%; Score 95.4; DB 8; Length 1001;
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Matches 111; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Qy 1234 GAGAGATCTCTAAAGAGATTTATCGTTTCAAGTAAGTCTCTTTATCAAACTTTAATATA 1293
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Qy 1294 AACAAATCAAAACATCA 1310
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Db 121 ATTAACAACAAAAAGA 137

RESULT 9
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ACCESSION
CR382399.1 AL844505
VERSION
CR382399.1 GI:46361038
KEYWORDS
HTG.
SOURCE
Plasmodium falciparum 3D7
ORGANISM
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 348174)
Hall,N., Pain,A., Berriman,M., Churcher,C., Harris,B., Harris,D.,
Mungall,K., Bowman,S., Atkin,R., Baker,S., Barron,A., Brooks,K.,
Buckee,C.O., Burrows,C., Cherevach,I., Chillingworth,C.,
Chillingworth,T., Christodoulou,Z., Clark,L., Clark,R., Corton,C.,
Cronin,A., Davies,R., Davis,P., Dear,P., Dearden,F., Doggett,J.,
Feltwell,T., Goble,A., Goodhead,I., Gwilliam,R., Hamlin,N.,
Hance,Z., Harper,D., Hauser,H., Hornsby,T., Holroyd,S.,
Horrocks,P., Humphray,S., Jagels,K., James,K.D., Johnson,D.,
Kerhornou,A., Knights,A., Konfortov,B., Kyes,S., Larkin,N.,
Lawson,D., Lennard,N., Line,A., Maddison,M., McLean,J., Mooney,P.,
Moule,S., Murphy,L., Oliver,K., Ormond,D., Price,C., Quail,M.A.,
Rabinovitch,E., Rajandream,M.A., Rutter,S., Rutherford,K.M.,
Sanders,M., Simmonds,M., Seeger,K., Sharp,S., Smith,R., Squares,R.,
Squares,S., Stevens,K., Taylor,K., Tivey,A., Unwin,L.,

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Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and Barrell, B.G.  
 Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13  
 Nature 419 (6906), 527-531 (2002)  
 22255708  
 MEDLINE  
 PUBMED  
 12368867  
 2 (bases 1 to 348174)  
 Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K., Berriman, M., Pain, A., Hall, N., Atkin, R., Chillingworth, C., Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M. and Barrell, B.G.  
 Unpublished  
 3 (bases 1 to 348174)  
 Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K., Berriman, M., Pain, A., Hall, N., Atkin, R., Chillingworth, C., Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M. and Barrell, B.G.  
 Direct Submission  
 Submitted (20-SEP-2002) P. falciparum Genome Sequencing Consortium, The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK  
 4 (bases 1 to 348174)  
 Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K., Berry, A.E., Berriman, M., RA Pain, A., Hall, N., Atkin, R., Chillingworth, C., Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M. and Barrell, B.G.  
 Direct Submission  
 Submitted (26-MAR-2004) P. falciparum Genome Sequencing Consortium, The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK  
 For more information about this sequence or the Malaria Project, see [http://www.sanger.ac.uk/Projects/P\\_falciparum](http://www.sanger.ac.uk/Projects/P_falciparum).  
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Db

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other sequences; artificial sequences.
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REFERENCE
AUTHORS
Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
Olsek,A., Piepenbrock,C., Aadorjan,P., Grabs,G., Lesche,R., Leu,E.,
Lewin,A., Lipscher,E., Mater,S., Model,F., Mueller,V., Otto,T.,
Pellet,C. and Ziebarth,H.
TITLE
Methods and nucleic acids for the analysis of hematopoietic cell
proliferative disorders
JOURNAL
Patent: WO 02077272-A 386 03-OCT-2002;
Epigenomics AG (DE)
FEATURES
Location/Qualifiers
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DB	25185	TAAATTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	25244
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DEPT. T 15

RESULT IS  
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ACT 19.

LOCUS

AC110300

26565 bn

DN

linear

6-APR-2002

26365 bp DNA IMAGEZ 11C 20 1111  
e 19 clone I.I.NI.19EOS-21E4. WORKING DRAFT

SEQUENCE, 2 unordered pieces.  
AC119399  
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HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 26565)  
DOE Joint Genome Institute.  
TITLE Sequencing of Human Chromosome 19  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 26565)  
DOE Joint Genome Institute.  
Direct Submission  
Submitted (26-APR-2002) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>  
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Project Information  
Center Project Name: 32002, FOS36972  
Center clone name: LLNL-FOS\_21E4  
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Summary Statistics  
Consensus quality: 23959 bases at least Q40  
Consensus quality: 25069 bases at least Q30  
Consensus quality: 25752 bases at least Q20  
Estimated insert size: 43700; agarose-fp estimation  
Estimated insert size: 26465; sum-of-contigs estimation  
Quality coverage: 8.47 in Q20 bases; agarose-fp estimation  
Quality coverage: 13.99 in Q20 bases; sum-of-contigs estimation.  
NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 2369: contig of 2369 bp in length  
\* 2370 2465: gap of unknown length  
\* 2470 26565: contig of 24096 bp in length.  
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/db\_xref="taxon:9606"  
/chromosome="19"  
/clone="LLNL19FOS-21E4"  
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Best Local Similarity 45.8%; Pred. No. 0.00027;  
Matches 342; Conservative 0; Mismatches 403; Indels 1; Gaps 1;  
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DB 5929 ATATATTAATTACATAAAGCTGTATTAATAATATAATAATATAATATAATATAATATAATATAT 5870  
QY 73 ATTACAAAAGGAAAAAATAATTTTTTGATCTCTAAAGTTATAACTTACAAATTTTCC 132  
DB 5869 AATATACTAATAATAATTTATATAATAATTTATATATATATATATATATATATATATAATTTA 5810  
QY 133 ACATCTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAGTTTCGGTTTAGGAAAA 192  
DB 5809 TTATATATATAGTATATAAATAAATTTATTTATATATATATATATATATATATATATA 5750  
QY 193 TGTATCTTTTTCATATAAAAAATATAGATCTTCAAGAAACTGAATTTGGTTTCAACT 252  
DB 5749 TATAATATATATAATATGTAATATATAATAATAATAATAATAATAATAATAATAATAATA 5690

QY 253 ATTTTATCGTTTGACACTACTTTTGACTTATCAAAAAGAGTTTCAAAATAGAAAAATAGAAT 312  
DB 5689 ATTATATAAAATTTATATATCAATTTATTTATTAATAATTTATATATATATATATATATATAGTTATGT 5630  
QY 313 CGAATCACACGTTTTCAGTGTGAAGAGGGAATTTGATATTTGGTCGACATTTTAAAGAGTTGTT 372  
DB 5629 ATAAATTATATTTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAT 5570  
QY 373 TTGTTTTTTTTTCCAAATCTGCATCGGTTTTCGGTTCCGTTGAACCAAAATTCACACATTTGT 432  
DB 5569 ATATAAATAATTTATATACCTATATATATATAATTTATATAATAATAATAATAATAATAATA 5510  
QY 433 ATAAACGGATAGTAAATATACTAGAGCTAGCGCAATACCAAAAAATAAAATTAACACTCAA 492  
DB 5509 CATATAATTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 5450  
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Search completed: October 24, 2005, 00:50:34  
Job time : 8766 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: October 23, 2005, 14:50:52 ; Search time 1093 Seconds  
(without alignments)  
10994.579 Million cell updates/sec

Title: US-10-643-676-1  
Perfect score: 2030  
Sequence: 1 cttcatgaagatggacca.....tttagattaaacaacaaaag 2030

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: geneseqn1990s:  
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4: geneseqn2001s:  
5: geneseqn2001bs:  
6: geneseqn2002s:  
7: geneseqn2002bs:  
8: geneseqn2003s:  
9: geneseqn2003bs:  
10: geneseqn2003cs:  
11: geneseqn2003ds:  
12: geneseqn2004s:  
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	2030	100.0	2042	6	ABZ75216	Arabidops
3	1064	52.4	1064	6	ABZ16347	Arabidops
4	95.4	4.7	999	3	AAC49043	Arabidops
5	95.4	4.7	1001	3	AAC37034	Arabidops
6	93.4	4.6	495	3	AAC38110	Arabidops
7	90.2	4.4	8056	8	ABZ10246	Haematopo
8	88.4	4.4	115218	8	ACA64845	Human HNR
9	87.4	4.3	515	3	AAC52118	Arabidops
10	82.8	4.1	8056	8	ABZ10100	Haematopo
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13	76	3.7	9810	6	ABL32426	Human imm
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17	74.2	3.7	5413	4	AAS46694	Tumour su
18	73.2	3.6	6242	6	ABL34148	Human imm
19	72.4	3.6	19634	8	ABZ10015	Haematopo
20	72.4	3.6	19634	8	ABZ10161	Haematopo

C 21	72.4	3.6	19634	13	ADS89671	Ad89671 Oligonuc1
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C 23	72.2	3.5	478	13	ACN51993	Acn51993 Cotton an
C 24	72	3.5	10682	6	ABN80085	Abn80085 Human che
C 25	71.8	3.5	8056	8	ABZ10100	Abz10100 Haematopo
C 26	71.8	3.5	110000	6	ABA92787_3	Continuation (4 of
C 27	71.4	3.5	883	4	AAL15210	Aal15210 Human bre
C 28	71.4	3.5	960	11	ACN85231	Acn85231 Breast ca
C 29	71	3.5	529	13	ACN56029	Acn56029 Cotton an
C 30	71	3.5	1501	8	ABZ10188	Abz10188 Haematopo
C 31	71	3.5	1501	10	ADE84162	Ade84162 Human lym
C 32	70.8	3.5	5979	4	AAS45313	Aas45313 Chemical
C 33	70.8	3.5	5979	6	ABK28152	Abk28152 DNA trans
C 34	69.4	3.4	11964	6	ABQ67025	Abq67025 Human ang
C 35	69.4	3.4	158001	12	ADL17884	Adl17884 Human pho
C 36	69.2	3.4	110000	13	ABD32968_6	Continuation (7 of
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C 38	69	3.4	13286	13	ADS89730	Ad889730 Oligonuc1
C 39	68.8	3.4	7498	6	ABL32257	Ab132257 Human imm
C 40	68.8	3.4	19787	6	ABL33451	Ab133451 Human imm
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C 42	68.8	3.4	20420	6	ABK69933	Abk69933 Human sec
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C 44	68.2	3.4	14023	6	ABL34105	Ab134105 Human imm
C 45	67.8	3.3	6071	6	ABL32325	Ab132325 Human imm

## ALIGNMENTS

RESULT 1  
ABZ75215  
ID ABZ75215 standard; cDNA; 2030 BP.  
XX  
AC ABZ75215;  
XX  
DT 23-APR-2003 (first entry)  
XX  
DE Arabidopsis thaliana endomembrane associated promoter cDNA.  
XX  
KW ENDO; endomembrane associated; promoter; expression; gene; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN W0200268665-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 14-FEB-2002; 2002WO-EP002894.  
XX  
PR 22-FEB-2001; 2001US-0270779P.  
XX  
PA (RHOB-) RHOBIO.  
XX  
PI Thomas T, Nuccio M, Hsieh T;  
XX  
DR WPI; 2002-707007/76.  
XX  
PT New isolated ENDO promoter from the gene of Arabidopsis thaliana, useful  
PT for directing expression of genes in plants.  
XX  
PS Claim 1; Page 17; 18pp; English.  
XX  
CC The invention relates to the novel isolated Arabidopsis thaliana  
CC endomembrane associated (ENDO) gene promoter sequence. The nucleic acid  
CC is useful for directing expression of genes in plants. The present  
CC sequence represents the A. thaliana ENDO promoter of the invention  
XX  
SQ Sequence 2030 BP; 722 A; 287 C; 319 G; 702 T; 0 U; 0 Other;  
Query Match 100.0%; Score 2030; DB 6; Length 2030;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 841 ACGTTTTTACCCCTTCTCTCTGTTTTCAGCGTTTAAATTTCAATTTTACTATTTGTACCGCT 900
Qy 901 GTCTTTTCACTTTTAAAGAAAAACCCAAACCGAAATCATAACTATACCGAAATCACAATGT 960
Db 901 GTCTTTTCACTTTTAAAGAAAAACCCAAACCGAAATCATAACTATACCGAAATCACAATGT 960
Qy 961 CTTTCATGGTCAGCTAACAAGACTTTATTTTCCGGTTGAAATTTGGTTTAACTATTGAGATT 1020
Db 961 CTTTCATGGTCAGCTAACAAGACTTTATTTTCCGGTTGAAATTTGGTTTAACTATTGAGATT 1020
Qy 1021 GTGCTAACCGAAAAACAGAAACGGTTATGACGCCAACGAGGCAAGAGGGGTAAAAACGAGAA 1080
Db 1021 GTGCTAACCGAAAAACAGAAACGGTTATGACGCCAACGAGGCAAGAGGGGTAAAAACGAGAA 1080
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## RESULT 2

ABZ75216

ID ABZ75216 standard; cDNA; 2042 BP.

XX ABZ75216;

XX ABZ75216;

DT 23-APR-2003 (first entry)

XX

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Qy 1081 AGAGGGGATGGCAGAAATCGTAAATTAACAGGAAAAATAAAGGGTGGTTTTCACGATAAGTC 1140
Db 1081 AGAGGGGATGGCAGAAATCGTAAATTAACAGGAAAAATAAAGGGTGGTTTTCACGATAAGTC 1140
Qy 1141 TGTCTATATGACCGCGAAAGGGTTTCTTAAATTCAGAGAGACAATTAATCAGTTTCGTGTG 1200
Db 1141 TGTCTATATGACCGCGAAAGGGTTTCTTAAATTCAGAGAGACAATTAATCAGTTTCGTGTG 1200
Qy 1201 TTTGGAGAGAAAGAAAGACAAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTATCGTT 1260
Db 1201 TTTGGAGAGAAAGAAAGACAAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTATCGTT 1260
Qy 1261 TCAAGTAAGTCTCTTTATCAAACTCTTAAATATAAACAATCAAAACATGAACACGTCGTG 1320
Db 1261 TCAAGTAAGTCTCTTTATCAAACTCTTAAATATAAACAATCAAAACATGAACACGTCGTG 1320
Qy 1321 TCTTCGTTTCGATTTCTAGATACGATTTTTCAGTTCATGTGAATGAACCTCTGTTTTATTAC 1380
Db 1321 TCTTCGTTTCGATTTCTAGATACGATTTTTCAGTTCATGTGAATGAACCTCTGTTTTATTAC 1380
Qy 1381 TACTAGGGTTGTTCAATATATTTTCCGAGAAATTAACGAGGAAACAAAGTTAGTGATTATAT 1440
Db 1381 TACTAGGGTTGTTCAATATATTTTCCGAGAAATTAACGAGGAAACAAAGTTAGTGATTATAT 1440
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Db 1441 TGATGCAGAGTATGAAGTAAATATATACATAAATCATGTTTCTCTCAAGCATCTACGT 1500
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Db 1681 ATTTTGTGCGCATGGCAATTTATGTCGAGGTAAAAATATACCAATAGAAACATATTTTGA 1740
Qy 1741 GGAGTAGTTAAGATTTAGATTGAAGAAATATCTATTACGATAAGCATAAATTTTCTTTTG 1800
Db 1741 GGAGTAGTTAAGATTTAGATTGAAGAAATATCTATTACGATAAGCATAAATTTTCTTTTG 1800
Qy 1801 CTGCTCTTGGTTTTTCTGTTTTATAGAACATTTGAATATGTAATTTGTTTTTTTTCACC 1860
Db 1801 CTGCTCTTGGTTTTTCTGTTTTATAGAACATTTGAATATGTAATTTGTTTTTTTTCACC 1860
Qy 1861 AGTAGATATGTACTATACACACAATAAGTAACATGGGTAGTTTATATAGAGAGAGATTGA 1920
Db 1861 AGTAGATATGTACTATACACACAATAAGTAACATGGGTAGTTTATATAGAGAGAGATTGA 1920
Qy 1921 TTTTTCGTAATATTTCTTTTGTGAAAAATAAATGATGTGTAATAATTTATGTTTATTATTT 1980
Db 1921 TTTTTCGTAATATTTCTTTTGTGAAAAATAAATGATGTGTAATAATTTATGTTTATTATTT 1980
Qy 1981 GACAGATTTGTTCCACGTTGAGAAAGTTTAAATTTAGATTAAACCAACAAAAAG 2030
Db 1981 GACAGATTTGTTCCACGTTGAGAAAGTTTAAATTTAGATTAAACCAACAAAAAG 2030
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QY 1621 CTCTCTTTGTCGGATTAGGTTAGGTTGGACTCAGAAATCAAAATACGATTAGCATACAA 1680  
DB 1627 CTCTCTTTGTCGGATTAGGTTAGGTTGGACTCAGAAATCAAAATACGATTAGCATACAA 1686  
QY 1681 ATTTTGGCATGGCAATTAATGTTCTGACGTTAAATATATACCAATAGAAACATATTTTA 1740  
DB 1687 ATTTTGGCATGGCAATTAATGTTCTGACGTTAAATATATACCAATAGAAACATATTTTA 1746  
QY 1741 GGAGTAGTAAAGTATGATGAAGAAATACTATTACGATAAGCATAAAATTTCTTTTG 1800  
DB 1747 GGAGTAGTAAAGTATGATGAAGAAATACTATTACGATAAGCATAAAATTTCTTTTG 1806  
QY 1801 CTGTTCTTGGTTTGTGCTTTTATAGAACATTCGAATATGCTACTTTTGTGTTTTTTCACC 1860  
DB 1807 CTGTTCTTGGTTTGTGCTTTTATAGAACATTCGAATATGCTACTTTTGTGTTTTTTCACC 1866  
QY 1861 AGTAGATATGCTACTATACACATAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1920  
DB 1867 AGTAGATATGCTACTATACACATAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1926  
QY 1921 TTTTTCGTATATTTCTTTGTTGAAATTAATATGCTAAATTTATGTTTATTAATTT 1980  
DB 1927 TTTTTCGTATATTTCTTTGTTGAAATTAATATGCTAAATTTATGTTTATTAATTT 1986  
QY 1981 GACAGATTGTTGCTGAGTAAAGTAAATTTAGATTAAACAAACAAAG 2030  
DB 1987 GACAGATTGTTGCTGAGTAAAGTAAATTTAGATTAAACAAACAAAG 2036

RESULT 3  
ABZ16347  
ID ABZ16347 standard; DNA; 1064 BP.  
XX  
AC ABZ16347;  
XX  
DT 21-JAN-2003 (first entry)  
XX  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4152.  
XX  
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
XX  
OS Arabidopsis thaliana.  
XX  
PN W0200216655-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 24-AUG-2001; 2001WO-US026685.  
XX  
PR 24-AUG-2000; 2000US-0227866P.  
PR 26-JAN-2001; 2001US-0264647P.  
PR 22-JUN-2001; 2001US-0300111P.  
XX  
PA (SCRI ) SCRIPPS RES INST.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Harper JF, Kreps J, Wang X, Zhu T;  
XX  
DR WPI; 2002-304127/34.  
XX  
PT Identifying a stress condition to which a plant cell has been exposed and  
PT producing plants with increased tolerance to these abiotic stresses.  
XX  
PS Claim 14; SEQ ID NO 4152; 577pp + Sequence Listing; English.  
XX  
CC The invention relates to identifying a stress condition to which a plant  
CC cell has been exposed, comprising: (a) contacting nucleic acid  
CC representative of expressed polynucleotides in the plant cell with an  
CC array or probes representative of the plant cell genome; and (b)  
CC detecting a profile of expressed polynucleotides in the plant cell  
CC characteristic of a stress response. The method is useful in the  
CC production of transgenic plants, cells and seeds and in producing plants  
CC with increased tolerance to abiotic stress. The present sequence is that

CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used  
CC in methods of the invention. Note: The sequence data for this patent is  
CC not represented in the printed specification but is based on sequence  
CC information supplied to Derwent by the European Patent Office  
XX  
SQ Sequence 1064 BP; 375 A; 126 C; 197 G; 366 T; 0 U; 0 Other;  
Query Match 52.4%; Score 1064; DB 6; Length 1064;  
Best Local Similarity 100.0%; Pred. No. 3.4e-170; Indels 0; Gaps 0;  
Matches 1064; Conservative 0; Mismatches 0;  
QY 967 GGTGACGTAAACAGACTTAATTTCCGGTTGAAATTTGGTTTAACTATTGAGATTGGCTA 1026  
DB 1 GGTGACGTAAACAGACTTAATTTCCGGTTGAAATTTGGTTTAACTATTGAGATTGGCTA 60  
QY 1027 ACCGAAAAACAGAAACGGTTATGACGCCAACGAGGCAAGGGGTAAACAGAAAGAGG 1086  
DB 61 ACCGAAAAACAGAAACGGTTATGACGCCAACGAGGCAAGGGGTAAACAGAAAGAGG 120  
QY 1087 GATGGCAGAAATCGTAATTAACAGGAAATAAAGGTTGGTTTACGATAAGTCTGTCTA 1146  
DB 121 GATGGCAGAAATCGTAATTAACAGGAAATAAAGGTTGGTTTACGATAAGTCTGTCTA 180  
QY 1147 TATGACGCCGAAAGGGTTTCTTAAATTCAGAGACAAATTAATCAGTTTCGTGTGTTGGA 1206  
DB 181 TATGACGCCGAAAGGGTTTCTTAAATTCAGAGACAAATTAATCAGTTTCGTGTGTTGGA 240  
QY 1207 GAAGAAGAAACAGATCAAAATACGAGGAGATCTCTAAAGAGATTATCGTTTCAAGT 1266  
DB 241 GAAGAAGAAACAGATCAAAATACGAGGAGATCTCTAAAGAGATTATCGTTTCAAGT 300  
QY 1267 AAGTCTCTTTATCAAACTCTTAATATATAAACAATCAAAACATCAACACGTCGTCTTCG 1326  
DB 301 AAGTCTCTTTATCAAACTCTTAATATATAAACAATCAAAACATCAACACGTCGTCTTCG 360  
QY 1327 TTTTCGATTCTAGATACGATTTTTTTAGTTTCATGTAATGAACCTCTGTTTATTACTACTAG 1386  
DB 361 TTTTCGATTCTAGATACGATTTTTTTAGTTTCATGTAATGAACCTCTGTTTATTACTACTAG 420  
QY 1387 GGTGTTTCAATATTTTCGAGAAATTAACGAGGAAACAAAGTTAGTGATTATATTGATGC 1446  
DB 421 GGTGTTTCAATATTTTCGAGAAATTAACGAGGAAACAAAGTTAGTGATTATATTGATGC 480  
QY 1447 AGAGTATGAAGTAAATATATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAAT 1506  
DB 481 AGAGTATGAAGTAAATATATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAAT 540  
QY 1507 ATATATAAGAAAGTTTTTTTTTGGTGAATAATATGTATGAGAAAGTTCACTTTTCAATAA 1566  
DB 541 ATATATAAGAAAGTTTTTTTTTGGTGAATAATATGTATGAGAAAGTTCACTTTTCAATAA 600  
QY 1567 GTGAAACAACTCTCTTTTCATACCAAAAAAATTTGAAAAAATTTAGTGAACCTCTCT 1626  
DB 601 GTGAAACAACTCTCTTTTCATACCAAAAAAATTTGAAAAAATTTAGTGAACCTCTCT 660  
QY 1627 TTCTCCGATTAGGTTAGGTTTGGACTCAGAATCAAAATACGATTAGCATAAACAAATTTT 1686  
DB 661 TTCTCCGATTAGGTTAGGTTTGGACTCAGAATCAAAATACGATTAGCATAAACAAATTTT 720  
QY 1687 TGGCATGGCAATTAATGTTCTGACGTTAAATATACCAATAGAAACATATTTTGGAGTA 1746  
DB 721 TGGCATGGCAATTAATGTTCTGACGTTAAATATACCAATAGAAACATATTTTGGAGTA 780  
QY 1747 GTTAAGATTATGATTGAAGAAATACTATTACGATAAGCATAAAATTTCTTTTCTGTGTT 1806  
DB 781 GTTAAGATTATGATTGAAGAAATACTATTACGATAAGCATAAAATTTCTTTTCTGTGTT 840  
QY 1807 TTGTTTTTGTCTCTTTTATAGAAATTTGAATATGTTTGTGTTTTTTCACCAGTAGA 1866  
DB 841 TTGTTTTTGTCTCTTTTATAGAAATTTGAATATGTTTGTGTTTTTTCACCAGTAGA 900  
QY 1867 TATGTACTATACACATTAAGTAACTGGGTAGTTTATATAGAGAGATTGATTTTTC 1926

Db 901 TATGCTACTATACACATAAGTAACATGGGTAGTGTATATAGAGAGAGATTGATTTTC 960  
Qy 1927 GTATATTTCTTTGTTGAAATAAATATGTAATAATTTATGTTTATTTGACAGA 1986  
Db 961 GTATATTTCTTTGTTGAAATAAATATGTAATAATTTATGTTTATTTGACAGA 1020  
Qy 1987 TTTGTTCCAGCTTGAGAAGTTTAATTTAGATTAAACACAAACAAAG 2030  
Db 1021 TTTGTTCCAGCTTGAGAAGTTTAATTTAGATTAAACACAAACAAAG 1064

RESULT 4  
AAC49043  
ID AAC49043 standard; DNA; 999 BP.  
XX AAC49043;  
XX 18-OCT-2000 (first entry)  
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 59714.  
XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
XX Arabidopsis thaliana.

XX EP1033405-A2.  
XX 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-00301439.  
XX 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
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PR 16-APR-1999; 99US-0129845P.  
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Best Local Similarity 81.0%; Pred. No. 5.5e-07;						
Matches 111; Conservative 0; Mismatches 26; Indels 0; Gaps 0;						
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QY	1234	GAGAGATCTCTAAAGAGAGATTATCGTTTCAAGTAAGTCTCTTTTATCAAACTCTTAATATA	1293
Db	61	GAGAGATCTCTAAAGAGAGATTATCGTTTCAAAATTTGTTTCACGTTGAGAAGTTTAATTAG	120
QY	1294	AACAAATCAAAACATGA	1310
Db	121	ATTAACAACAACAAAAGA	137
RESULT 5			
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ID	AAC37034 standard; DNA; 1001 BP.		
XX	AAC37034;		
AC			
XX			
DT	17-OCT-2000 (first entry)		
XX			
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 15944.		
XX			
KW	Hybridisation assay; genetic mapping; gene expression control;		
KW	protein identification; signal transduction pathway; metabolic pathway;		
KW	promoter; termination sequence; ss.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	EP1033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-00301439.		
XX			
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PR	29-MAR-1999;	99US-0126785P.	
PR	01-APR-1999;	99US-0127462P.	
PR	06-APR-1999;	99US-0128234P.	
PR	08-APR-1999;	99US-0128714P.	
PR	16-APR-1999;	99US-0129845P.	
PR	19-APR-1999;	99US-0130077P.	
PR	21-APR-1999;	99US-0130449P.	
PR	23-APR-1999;	99US-0130510P.	
PR	23-APR-1999;	99US-0130891P.	
PR	28-APR-1999;	99US-0131449P.	
PR	30-APR-1999;	99US-0132048P.	
PR	30-APR-1999;	99US-0132407P.	
PR	04-MAY-1999;	99US-0132484P.	
PR	05-MAY-1999;	99US-0132485P.	
PR	06-MAY-1999;	99US-0132486P.	
PR	06-MAY-1999;	99US-0132487P.	
PR	07-MAY-1999;	99US-0132863P.	
PR	11-MAY-1999;	99US-0134256P.	
PR	14-MAY-1999;	99US-0134218P.	
PR	14-MAY-1999;	99US-0134219P.	
PR	14-MAY-1999;	99US-0134221P.	
PR	14-MAY-1999;	99US-0134370P.	
PR	18-MAY-1999;	99US-0134768P.	
PR	19-MAY-1999;	99US-0134941P.	
PR	20-MAY-1999;	99US-0135124P.	
PR	21-MAY-1999;	99US-0135353P.	
PR	24-MAY-1999;	99US-0135629P.	
PR	25-MAY-1999;	99US-0136021P.	
PR	27-MAY-1999;	99US-0136392P.	
PR	28-MAY-1999;	99US-0136782P.	
PR	01-JUN-1999;	99US-0137222P.	
PR	03-JUN-1999;	99US-0137528P.	
PR	04-JUN-1999;	99US-0137502P.	
PR	07-JUN-1999;	99US-0137724P.	

PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
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PR 17-JUN-1999; 99US-0139492P.  
PR 17-JUN-1999; 99US-0139494P.  
PR 18-JUN-1999; 99US-0139454P.  
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PR 18-JUN-1999; 99US-0139459P.  
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PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144082P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
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PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
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PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
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PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.

PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 18-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160769P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160982P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match

4.7%; Score 95.4; DB 3; Length 1001;

Best Local Similarity 81.0%;

Matches 111; Conservative 0; Mismatches 26;

Indels

0;

Gaps

0;

Qy	1174	AGAGAGACAATTAATCATGTTTCGTGCTGTTGGAGAAGAAGAACAGATCAAAATACGAG	1233	PR	07-JUN-1999;	99US-0137724P.
Db	1	AGAGAGACAATTAATCATGTTTCGTGCTGTTGGAGAAGAAGAACAGATCAAAATACGAG	60	PR	08-JUN-1999;	99US-0138094P.
Qy	1234	GAGAGATCTCTAAAGAGATTATCGTTTCAAGTAACTCTTTATCAAACTCTTAATATA	1293	PR	10-JUN-1999;	99US-0138540P.
Db	61	GAGAGATCTCTAAAGAGATTATCGTTTCAAAATTTGTCAGGTGAGAGTTTAATTAG	120	PR	14-JUN-1999;	99US-0139119P.
Qy	1294	AACAAATCAAAACATGA	1310	PR	16-JUN-1999;	99US-0139452P.
Db	121	ATTAACAACAACAAAAGA	137	PR	17-JUN-1999;	99US-0139453P.
RESULT 6				PR	18-JUN-1999;	99US-0139454P.
ID	AAC38110	standard; DNA; 495 BP.		PR	18-JUN-1999;	99US-0139455P.
AC	AAC38110;			PR	18-JUN-1999;	99US-0139456P.
XX				PR	18-JUN-1999;	99US-0139457P.
DT	17-OCT-2000	(first entry)		PR	18-JUN-1999;	99US-0139458P.
XX				PR	18-JUN-1999;	99US-0139459P.
DE	Arabidopsis thaliana	DNA fragment SEQ ID NO: 19822.		PR	18-JUN-1999;	99US-0139460P.
XX				PR	18-JUN-1999;	99US-0139461P.
KW	Hybridisation assay; genetic mapping; gene expression control;			PR	18-JUN-1999;	99US-0139462P.
KW	protein identification; signal transduction pathway; metabolic pathway;			PR	18-JUN-1999;	99US-0139463P.
KW	promoter; termination sequence; ss.			PR	18-JUN-1999;	99US-0139750P.
XX				PR	18-JUN-1999;	99US-0139763P.
OS	Arabidopsis thaliana.			PR	21-JUN-1999;	99US-0139817P.
XX				PR	22-JUN-1999;	99US-0139899P.
PN	EPI033405-A2.			PR	23-JUN-1999;	99US-0140353P.
XX				PR	23-JUN-1999;	99US-0140354P.
PD	06-SEP-2000.			PR	24-JUN-1999;	99US-0140695P.
XX				PR	28-JUN-1999;	99US-0140823P.
PF	25-FEB-2000; 2000EP-00301439.			PR	29-JUN-1999;	99US-0140991P.
XX				PR	30-JUN-1999;	99US-0141287P.
PR	25-FEB-1999;	99US-0121825P.		PR	01-JUL-1999;	99US-0141287P.
PR	05-MAR-1999;	99US-0121825P.		PR	02-JUL-1999;	99US-0141287P.
PR	09-MAR-1999;	99US-0123548P.		PR	02-JUL-1999;	99US-0142055P.
PR	23-MAR-1999;	99US-0123548P.		PR	06-JUL-1999;	99US-0142190P.
PR	29-MAR-1999;	99US-0126264P.		PR	08-JUL-1999;	99US-0142803P.
PR	01-APR-1999;	99US-0126785P.		PR	09-JUL-1999;	99US-0142920P.
PR	06-APR-1999;	99US-0127462P.		PR	12-JUL-1999;	99US-0142977P.
PR	08-APR-1999;	99US-0128234P.		PR	13-JUL-1999;	99US-0143542P.
PR	16-APR-1999;	99US-0128714P.		PR	14-JUL-1999;	99US-0143624P.
PR	19-APR-1999;	99US-0129845P.		PR	15-JUL-1999;	99US-0144005P.
PR	21-APR-1999;	99US-0130077P.		PR	16-JUL-1999;	99US-0144086P.
PR	23-APR-1999;	99US-0130510P.		PR	19-JUL-1999;	99US-0144325P.
PR	28-APR-1999;	99US-0131449P.		PR	19-JUL-1999;	99US-0144331P.
PR	30-APR-1999;	99US-0132048P.		PR	19-JUL-1999;	99US-0144332P.
PR	04-MAY-1999;	99US-0132407P.		PR	19-JUL-1999;	99US-0144332P.
PR	05-MAY-1999;	99US-0132484P.		PR	19-JUL-1999;	99US-0144332P.
PR	06-MAY-1999;	99US-0132485P.		PR	20-JUL-1999;	99US-0144632P.
PR	06-MAY-1999;	99US-0132486P.		PR	20-JUL-1999;	99US-0144632P.
PR	06-MAY-1999;	99US-0132487P.		PR	21-JUL-1999;	99US-0144814P.
PR	07-MAY-1999;	99US-0132863P.		PR	21-JUL-1999;	99US-0145086P.
PR	11-MAY-1999;	99US-0134256P.		PR	21-JUL-1999;	99US-0145088P.
PR	14-MAY-1999;	99US-0134218P.		PR	22-JUL-1999;	99US-0145087P.
PR	14-MAY-1999;	99US-0134219P.		PR	22-JUL-1999;	99US-0145089P.
PR	14-MAY-1999;	99US-0134221P.		PR	22-JUL-1999;	99US-0145192P.
PR	14-MAY-1999;	99US-0134370P.		PR	23-JUL-1999;	99US-0145145P.
PR	18-MAY-1999;	99US-0134768P.		PR	23-JUL-1999;	99US-0145218P.
PR	19-MAY-1999;	99US-0134941P.		PR	23-JUL-1999;	99US-0145224P.
PR	20-MAY-1999;	99US-0135124P.		PR	26-JUL-1999;	99US-0145276P.
PR	21-MAY-1999;	99US-0135353P.		PR	27-JUL-1999;	99US-0145913P.
PR	24-MAY-1999;	99US-0135629P.		PR	27-JUL-1999;	99US-0145918P.
PR	25-MAY-1999;	99US-0136021P.		PR	27-JUL-1999;	99US-0145919P.
PR	27-MAY-1999;	99US-0136382P.		PR	28-JUL-1999;	99US-0145951P.
PR	28-MAY-1999;	99US-0136782P.		PR	02-AUG-1999;	99US-0146386P.
PR	01-JUN-1999;	99US-0137222P.		PR	02-AUG-1999;	99US-0146386P.
PR	03-JUN-1999;	99US-0137528P.		PR	03-AUG-1999;	99US-0146389P.
PR	04-JUN-1999;	99US-0137502P.		PR	04-AUG-1999;	99US-0147038P.
PR				PR	04-AUG-1999;	99US-0147204P.
PR				PR	05-AUG-1999;	99US-0147302P.
PR				PR	05-AUG-1999;	99US-0147192P.
PR				PR	05-AUG-1999;	99US-0147260P.
PR				PR	06-AUG-1999;	99US-0147303P.



PR 06-AUG-1999;	99US-0147416P.	QY 1176	AGAGACAATTAATCAGTTTCGTGTTTGGAGAAAGAAAGACAGATCAATACGAGGA	1235
PR 09-AUG-1999;	99US-0147493P.	Db 1	AGAGACAATTAATCAGTTTCGTGTTTGGAGAAAGAAAGACAGATCAATACGAGGA	60
PR 09-AUG-1999;	99US-0147935P.	QY 1236	GAGATCTCTAAAGAGATTATCGTTTCAAGTAAGTCTCTTTATCAAACTCTTAATATAA	1295
PR 10-AUG-1999;	99US-0148171P.	Db 61	GAGATCTCTAAAGAGATTATCGTTTCAAAATTTGTTTCAAGTCTGTTTAAATTTAGAT	120
PR 11-AUG-1999;	99US-0148319P.	QY 1296	CAATCAAAACATCA	1310
PR 12-AUG-1999;	99US-0148341P.	Db 121	TAAACAACAAGA	135
PR 13-AUG-1999;	99US-0148565P.	RESULT 7		
PR 13-AUG-1999;	99US-0148684P.	ABZ10246/C		
PR 16-AUG-1999;	99US-0149368P.	ID ABZ10246	standard; DNA; 8056 BP.	
PR 17-AUG-1999;	99US-0149175P.	XX ABZ10246;		
PR 18-AUG-1999;	99US-0149426P.	XX 16-JAN-2003	(first entry)	
PR 20-AUG-1999;	99US-0149722P.	DT		
PR 20-AUG-1999;	99US-0149929P.	XX		
PR 23-AUG-1999;	99US-0149902P.	XX		
PR 23-AUG-1999;	99US-0149930P.	DE		
PR 25-AUG-1999;	99US-0150566P.	XX		
PR 26-AUG-1999;	99US-0150884P.	DE		
PR 27-AUG-1999;	99US-0151065P.	XX		
PR 27-AUG-1999;	99US-0151066P.	XX		
PR 27-AUG-1999;	99US-0151080P.	XX		
PR 30-AUG-1999;	99US-0151303P.	XX		
PR 31-AUG-1999;	99US-0151438P.	XX		
PR 01-SEP-1999;	99US-0151930P.	XX		
PR 07-SEP-1999;	99US-0152363P.	XX		
PR 10-SEP-1999;	99US-0153070P.	XX		
PR 13-SEP-1999;	99US-0153758P.	XX		
PR 15-SEP-1999;	99US-0154018P.	OS		
PR 16-SEP-1999;	99US-0154039P.	XX		
PR 20-SEP-1999;	99US-0154779P.	XX		
PR 22-SEP-1999;	99US-0155139P.	XX		
PR 23-SEP-1999;	99US-0155486P.	XX		
PR 24-SEP-1999;	99US-0155653P.	XX		
PR 28-SEP-1999;	99US-0156458P.	XX		
PR 29-SEP-1999;	99US-0156596P.	XX		
PR 04-OCT-1999;	99US-0157117P.	XX		
PR 05-OCT-1999;	99US-0157753P.	XX		
PR 06-OCT-1999;	99US-0157865P.	XX		
PR 07-OCT-1999;	99US-0158029P.	XX		
PR 08-OCT-1999;	99US-0158232P.	XX		
PR 12-OCT-1999;	99US-0158369P.	XX		
PR 13-OCT-1999;	99US-0159293P.	XX		
PR 13-OCT-1999;	99US-0159294P.	XX		
PR 13-OCT-1999;	99US-0159295P.	XX		
PR 14-OCT-1999;	99US-0159330P.	XX		
PR 14-OCT-1999;	99US-0159331P.	XX		
PR 14-OCT-1999;	99US-0159637P.	XX		
PR 14-OCT-1999;	99US-0159638P.	XX		
PR 18-OCT-1999;	99US-0159584P.	XX		
PR 21-OCT-1999;	99US-0160741P.	XX		
PR 21-OCT-1999;	99US-0160767P.	XX		
PR 21-OCT-1999;	99US-0160768P.	XX		
PR 21-OCT-1999;	99US-0160770P.	XX		
PR 21-OCT-1999;	99US-0160814P.	XX		
PR 21-OCT-1999;	99US-0160815P.	XX		
PR 22-OCT-1999;	99US-0160980P.	XX		
PR 22-OCT-1999;	99US-0160981P.	XX		
PR 22-OCT-1999;	99US-0160989P.	XX		
PR 25-OCT-1999;	99US-0161404P.	XX		
PR 25-OCT-1999;	99US-0161405P.	XX		
PR 25-OCT-1999;	99US-0161406P.	XX		
PR 26-OCT-1999;	99US-0161359P.	XX		
PR 26-OCT-1999;	99US-0161360P.	XX		
PR 26-OCT-1999;	99US-0161361P.	XX		
PR 28-OCT-1999;	99US-0161920P.	XX		
PR 28-OCT-1999;	99US-0161920P.	XX		
PR 28-OCT-1999;	99US-0161922P.	XX		
PR 29-OCT-1999;	99US-0161993P.	XX		
PR 29-OCT-1999;	99US-0162142P.	XX		

Query Match 4.6%; Score 93.4; DB 3; Length 495;  
Best Local Similarity 80.7%; Pred. No. 1.1e-06;  
Matches 109; Conservative 0; Mismatches 26; Indels 0; Gaps 0;







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PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 4.3%; Score 87.4; DB 3; Length 515;
Best Local Similarity 79.8%; Pred. No. 1.2e-05;
Matches 103; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1182 AATTAATCAGTTTCGTGTTGGAGAGAGAGAGACAGATCAATACGAGGAGAGATC 1241
Db 2 AATTAATCAGTTTCGTGTTGGAGAGAGAGAGACAGATCAATACGAGGAGAGATC 61

Qy 1242 TCTAAAGAGATTATCGTTTCAAGTAAGTCCTTTATCAAACTCTTAATATAACAAATC 1301
Db 62 TCTAAAGAGATTATCGTTTCAAAATTTGTCACGTTGAGAAAGTTTAATTTAGATTAAACA 121

Qy 1302 AAAACATGA 1310
Db 122 ACAAAGA 130

RESULT 10
ABZ10100/c
ID ABZ10100 standard; DNA; 8056 BP.
XX AC ABZ10100;
XX DT 16-JAN-2003 (first entry)
XX DE Haematopoietic cell proliferation disorder related DNA sequence #240.
XX KW Human; haematopoietic cell proliferation disorder; cytostatic;
XX KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
XX KW cytosine methylation state; gene; ds.
XX OS Homo sapiens.
XX FN WO200277272-A2.
XX PD 03-OCT-2002.
XX PF 26-MAR-2002; 2002WO-EP003401.
XX PR 26-MAR-2001; 2001US-0278333P.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Berlin K, Braun A, Distler J, Quetig D, Howe A, Mueller J;
XX PI Olek A, Plepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
XX PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
XX PI Schwöpe I, Ziebarth H;
XX DR WPI; 2003-018942/01.
XX PT Detecting and differentiating between hematopoietic cell proliferative
XX PT disorders, comprises contacting a target nucleic acid with a reagent that
XX PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX PS Claim 28; SEQ ID NO 240; 117pp; English.

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XX The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used; for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;

Query Match 4.1%; Score 82.8; DB 8; Length 8056;
Best Local Similarity 46.2%; Pred. No. 8.1e-05;
Matches 317; Conservative 0; Mismatches 362; Indels 7; Gaps 1;

Qy 36 TCTTTCTATTTTATTTGATTTAGAAAAATCATATTCATTACAAAGGAAAAAATA 95
Db 2063 TTTTAAAAAATAAAAAATATTTAAAAATATATTTTATTTTAAATATATTTTAA 2004

Qy 96 ATTTTGTATCTCTAAAGTTATACATTTTCCACACTTCAGTTGCTAGTATTAA 155
Db 2003 TTAAATTTTAAATAAAAAATAATTAATTAATTTTATTTTAAAAATATATTTT 1944

Qy 156 TTATCTATTTTATCAAGTTTGGTTTAGAAAAATGTATCTTTTCATATAAAAAATA 215
Db 1943 TTATATTAATTTAATTTATTTTATTTTATTAATAATTTTATTTTATATAAAAA 1884

Qy 216 TATAGATCTTCAAAAGAACTGAATTTGGTTTCAACTATTTTATCGTTTGACACTTTT 275
Db 1883 TAAAAATAATTAATTAATTTTATTTTATTTTATTTTATTTTAAAAACGAAATTT 1824

Qy 276 GACTTATCAAAAGAGTTTCAAAATAGAAAAATAGAAATCGAATCACAGTTTCAGTGAAG 335
Db 1823 TATTTTATTAATTAATTAATTAATTAATTAATTAATTTTATTTTATTTTAAATTA 1764

Qy 336 AGGATTTGATATTGGTCGACATTTTAAAGAGTTTGTGTTTGTGTTTTCCTCAATCTGCAT 395
Db 1763 AATTTTATTTTAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1704

Qy 396 GGTGTTTTCGTTTCGTTGAACCAAAATTCACACTTTTGTATAAACCGAATAGTAATACTA 455
Db 1703 TTAATTTTATAATTTTAAATAAAAAATAATTTTATCGTATTAATTAATAAATTTT 1644

Qy 456 GACGTACGCCAATACCAAAAAATAAAATTAACCTCAATTCACAAATTCGAATCTACACCAT 515
Db 1643 TAAATTTACGATTCGTTTATTTTCGATTTTAAAAATATTAATAATTAATAATAATA 1584

Qy 516 ATCA-----TGCATATATATCAGCAACCTFAGATAATCAATGAAATTTAATCGAGAT 568
Db 1583 AATATTAATTTAAATATAAATTTTAAAAAATAAATTTTATTTTAAAAATTTTAAACG 1524

Qy 569 AATCAATATCCAACCTCACGATAATCAAAAGCCTTAATTAATAGATCAATGAAATCAAAATA 628
Db 1523 TATTTATATTTTATATTTATATATATATTAATTAATTAATTAATTTTAAATTAATTT 1464

Qy 629 CTAACATAGTAATATACATTTGTTGTTTAAACAGAAATTAATATACATTAATAGATAT 688
Db 1463 ATTAATAAATAAATTTTATTTTATTTTATTTTAAAAAATAAATAAATAAATAAATAA 1404

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QY 689 GAAAAATGATATATATGAGATAGA 714  
DB 1403 ATCGATATTATTTTATAAAAAAA 1378

RESULT 11  
ID ABZ10246  
XX ABZ10246 standard; DNA; 8056 BP.  
AC ABZ10246;  
DT 16-JAN-2003 (first entry)  
XX Haematopoietic cell proliferation disorder related DNA sequence #386.  
DE Human; haematopoietic cell proliferation disorder; cytostatic;  
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
KW cytosine methylation state; gene; ds.  
XX Homo sapiens.  
OS WO200277272-A2.  
PN 03-OCT-2002.  
XX 26-MAR-2002; 2002WO-EP003401.  
XX 26-MAR-2001; 2001US-0278333P.  
XX (EPIG-) EPIGENOMICS AG.  
PA Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;  
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;  
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;  
PI Schwöbe I, Ziebarth H;  
XX WPI; 2003-018942/01.  
DR  
XX Detecting and differentiating between hematopoietic cell proliferative  
PT disorders, comprises contacting a target nucleic acid with a reagent that  
PT distinguishes between methylated and non-methylated CpG dinucleotides.  
XX Claim 28; SEQ ID NO 386; 117pp; English.  
XX The present invention describes a method for detecting and  
CC differentiating between haematopoietic cell proliferative disorders  
CC associated with at least 1 gene and/or their regulatory regions in a  
CC subject. The method comprises contacting a target nucleic acid in a  
CC biological sample obtained from the subject with at least 1 reagent,  
CC which distinguishes between methylated and non-methylated CpG  
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118  
CC represent specifically claimed nucleotide sequences from the present  
CC invention. Oligonucleotides from the present invention can be used for  
CC differentiating between healthy haematopoietic cells and proliferative  
CC disorder haematopoietic cells; for differentiating between acute  
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
CC determining the cytosine methylation state and/or single nucleotide  
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
CC related sequences and their complements; and as primers for the  
CC amplification of haematopoietic cell proliferation disorder related DNA  
CC sequences. The nucleotide sequences from the present invention can also  
CC be used for detecting a predisposition to, differentiation between  
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of  
CC haematopoietic cell proliferation disorders. The present method enables a  
CC highly specific classification of haematopoietic cell proliferative  
CC disorders allowing for improved and informed treatment of patients  
XX  
SQ Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;  
Query Match 3.9%; Score 79; DB 8; Length 8056;  
Best Local Similarity 45.4%; Pred. No. 0.00035;  
Matches 377; Conservative 0; Mismatches 440; Indels 14; Gaps 2;

QY 1162 TTCTTTAAATTCAGAGACAAATTAATCAGTTTCGTGTTGCGAAGAGAACAG 1221  
DB 269 TTATTTTAAATAAAAAAATTTTATTTTAAAAATTAATTTTAAAAAATAATTA 328  
QY 1222 ATCAAAATACGAGGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAGTCTCTTTATCAA 1281  
DB 329 TAAAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 388  
QY 1282 ACTCTTAATATAAAACAAACATGAACACGTCGTCTTCGTTTCGATCTAGATA 1341  
DB 389 ATTTAAAAATTTAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATA 448  
QY 1342 CGATTTTGTAGTTCATGTGAATGAACCTCTGTTTATTTACTACTAGGTTGTTCAATAATTT 1401  
DB 449 AAAAAAATTTAAATTTTAAAAAATAATAATAATAATAATAATAATAATAATAATAATA 508  
QY 1402 TTCGAGAAATTACCAGAGGAAACAAAGTTAGTGATTATATTGATGCAGAGTATGAAGTAAT 1461  
DB 509 TTTATAATATTA---AATATTATATTAATAATAATAATAATAATAATAATAATAATAATA 564  
QY 1462 TATATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAATATATATAAGAAGTTT 1521  
DB 565 GTTTTATTAATAATTAATTTATTAATAATAATAATAATAATAATAATAATAATAATAATTT 624  
QY 1522 TTTTGTGGTGAATAATATGATGAGAAGTTTCATCTTTCATAATAGTGAACAACCTCTCT 1581  
DB 625 TAAAAATTTTAAAAAATAATTTTAAATATATAATAATAATAATAATAATAATAATAATA 684  
QY 1582 TTCATACCAAAAAAATAATTTGAAAAAATAATAGTGAAACTCTCTTTGTCGAGTTAGGTT 1641  
DB 685 AATAATAAAAAAATTTTATATTTTAAATTTTAAATTTTAAATAATAATAATAATAATA 744  
QY 1642 AGGTTGGAATCAGAAATCAAAATACGATTAGCATACAAATTT-----TTTGGA 1691  
DB 745 ATTTTAAATTTTAAAAATTTAATAATAATAATAATAATAATAATAATAATAATAATAATA 804  
QY 1692 TGCAATTTATGTCGAGGTAAATAATATACCAATAGAAACATATTTTACGAGTAGTATA 1751  
DB 805 TAAATTTATAAATAGATTATTTAAATAATAATTTTATAATAATAATAATAATAATAATA 864  
QY 1752 GATTATGATTGAAGAAATACATATTACGATAAGCATAAAAATTTTCTTTGCTGTTTGGT 1811  
DB 865 TTTTATGATAAAAAATTTTGTAAATTTTAAATTTTATAATTTTAAATTTTGTGTTT 924  
QY 1812 TTTTGTGTTTTATAGAACATGCAATATGTAATGTAATTTTGTGTTTTTTTCCAGTAGATAAT 1871  
DB 925 TGTAAATAAATTTTAAAAAATAAATTTTATTTTATTTTAAATGAATAAATAATAT 984  
QY 1872 ACTATACACACATAAGTAACATGGTAGTTTATATAGAGAGAGATTGATTTTCGTATA 1931  
DB 985 ATTATAAATTTTAAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1044  
QY 1932 TTTCTTTGTGAAAAATAAATATGTAATAATTTATTTGTTTATTAATTTCA 1982  
DB 1045 ATTTAATTAATGTAATAATAAAAAAATTTGTTTAAATTTGTTTAAAA 1095

RESULT 12  
ID ABL34155/c  
XX ABL34155 standard; DNA; 15548 BP.  
AC ABL34155;  
XX  
XX 26-MAR-2002 (first entry)  
XX Human immune system associated gene SEQ ID NO: 2128.  
DE  
XX Human; immune system disease; cytosine methylation; antiasthmatic;  
KW antiarteriosclerotic; antianaemic; cytosine; cytosine; cytosine;  
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
KW



KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;	
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;	
KW	ds.	
OS	Homo sapiens.	
PN	WO200200928-A2.	
XX	03-JAN-2002.	
XX	02-JUL-2001; 2001WO-EP007537.	
XX	30-JUN-2000; 2000DE-01032529.	
PR	01-SEP-2000; 2000DE-01043826.	
XX	(EPIG-) EPIGENOMICS AG.	
PA	Olek A, Piepenbrock C, Berlin K;	
PI	WPI; 2002-130909/17.	
XX		
XX	Nucleic acid comprising fragment of chemically modified gene, useful for	
PT	diagnosis and treatment of diseases associated with abnormal cytosine	
PT	methylation.	
XX	Claim 1; SEQ ID NO 2128; 32pp + Sequence Listing; German.	
XX		
CC	The present invention provides a number of human immune system associated	
CC	genes which are modified by the methylation of cytosines. The sequences	
CC	can be used in the diagnosis and treatment of immune system disorders,	
CC	including eye diseases such as retinopathy, neovascular glaucoma and	
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid	
CC	leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,	
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel	
CC	diseases. The present sequence is a gene of the invention	
XX		
SQ	Sequence 15548 BP; 4209 A; 247 C; 2903 G; 8189 T; 0 U; 0 Other;	
Query Match 3.9%; Score 78.8; DB 6; Length 15548;		
Best Local Similarity 46.6%; Pred. No. 0.00039;		
Matches 324; Conservative 0; Mismatches 367; Indels 5; Gaps 2;		
Qy	62 AAATCATATTTCATCAAAAGGAAAAAATAATTTTGTGATCTCTAAAGTTTATAACT 121	
Db	12299 ATATAACATATATATATAAACATATATATAAACATATATATAAACATATATATAT 12240	
Qy	122 TACAAATTTCCACATTCAGTTGGTAGTATTAATTTATCTATTTTATCAAGTTTGGT 181	
Db	12239 AACATATATATATATAACATATATATAAACATATATATAAACATATATATAAACATA 12180	
Qy	182 TTTTAGGAAAAATCTATCTTTTCATATAAAAAATATATAGATCTTCAAAGAACTGAATTG 241	
Db	12179 TATATATAACATATATATATAACTTATAAAATAACATATATATAACATATAAAATAA 12120	
Qy	242 GGTTTTCAACTATTTTATCGTTTTGCACATCTTGACTTATCAAAAGAGTTCAAAATAG 301	
Db	12119 CATATAAAAAATAACATATAAAAAATAACATATAAAAAATAACATATAAAAAATAA 12060	
Qy	302 AAAAAATGAATCGAATCACACGTTCCAGTGTGAAGGGATTTGATATGGTTCGACATTTT 361	
Db	12059 AATAACATATAAAAAATAACATATAAAAAATAAAAAATAAAAAATAATATATAACATAT 12000	
Qy	362 AAAGAGTTGTTTTGTTTTTTTTTTTCCAACTCTGCATGGTTTTTTCGTTCCGTTGAACCAAAATT 421	
Db	11999 AAAAAATAAAATATATATAACATATAAAATAAATAATATATAACATATAAAAAATAACATA 11940	
Qy	422 CAACACCTTTGTATAAACCGGAATAGTAATATCTAGACGTACGCCAATACCAAAAAATAAAA 481	
Db	11939 TAAAAATAAAATATAAAAAATAAAATATAAAAAATAAAATAAATATAAAATATAAAAAATAA 11880	
Qy	482 TTAAAACTCAATTCCAAATTTGAATCTACACCATATCATGCAATATATATATCAGCAACTAG 541	
Db	11879 ATAAATATAAAATATAAAAAATAAAATAAAAAATAAAAAATAAAAAATAAAAAATAA 11820	





Qy 750 ATTACAAAT 758  
Db 5196 TATATATAT 5188

Search completed: October 23, 2005, 22:24:28  
Job time : 1099 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C	1	72.4	3.6	1141	4	US-09-806-708B-22
	2	72.2	3.6	18773	4	US-09-949-016-14164
	3	71.8	3.5	640681	4	US-09-790-988-1
	4	70.8	3.5	1141	4	US-09-806-708B-22
	5	70.8	3.4	205044	4	US-09-949-016-15851
	6	69.8	3.4	205044	4	US-09-949-016-15852
	7	69.8	3.4	205044	4	US-09-949-016-15853
	8	69.8	3.4	223471	4	US-09-949-016-12387
	9	69.8	3.4	223471	4	US-09-949-016-12724
	10	69.8	3.4	223471	4	US-09-949-016-13725
C	11	68.8	3.4	603176	4	US-09-949-016-16284
	12	68.8	3.4	603176	4	US-09-949-016-12423
	13	67.8	3.3	134987	4	US-09-949-016-15348
	14	67.8	3.3	134987	4	US-09-949-016-15349
	15	67.8	3.3	134987	4	US-09-949-016-15350
	16	67.8	3.3	134987	4	US-09-949-016-15507
	17	67.8	3.3	134987	4	US-09-949-016-15508
	18	67.8	3.3	134987	4	US-09-949-016-15509
	19	66	3.3	18773	4	US-09-949-016-14164
	20	65.2	3.2	114139	4	US-09-949-016-16536
C	21	65	3.2	30820	4	US-09-949-016-17145
	22	65	3.2	134987	4	US-09-949-016-15348
	23	65	3.2	134987	4	US-09-949-016-15349
	24	65	3.2	134987	4	US-09-949-016-15350
	25	65	3.2	134987	4	US-09-949-016-15507
	26	65	3.2	134987	4	US-09-949-016-15508
	27	65	3.2	134987	4	US-09-949-016-15509
	28	65	3.2	134987	4	US-09-949-016-15510
	29	65	3.2	134987	4	US-09-949-016-15511
	30	65	3.2	134987	4	US-09-949-016-15512







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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15851
; LENGTH: 205044
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(205044)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15851

Query Match      3.4%; Score 69.8; DB 4; Length 205044;
Best Local Similarity 46.3%; Pred. No. 0.00015;
Matches 305; Conservative 0; Mismatches 347; Indels 7; Gaps 2;

QY      72 CATTACAAAAGGAAAAAATAATTTTGTATCTCTAAAGTTTATAACTTACAAATTTTC 131
DB      200437 CAAAAATAAATCAAAATATATTTAAATATATACATTTATAGGTTATATCATCAAT 200496

QY      132 CACACTTCAGTTGGTAGTATTAATTTTATCTATTTTATCAAAAGTTTGGTTTAGGAAA 191
DB      200497 TTTATCAATATATTTAAATATAAATATATTTTAAATATATTTTAAATATAAATA 200556

QY      192 ATGTATCTTTTCATATAAAAAATATAGATCTTCAAGAAACTGAAATCGGTTTTCAC 251
DB      200557 ATATATTTATATATTTTAAATATAAATATATTTTAAATATAAATATATTTTAAAT 200615

QY      252 TATTTTATCGTTTGACACTCTTTGACTTATCAAAAAAGAGTTCAAAATAGAAAATAGAA 311
DB      200616 -----TATAAATATAAATAATATATTTTAAATATAAATATATTTTAAATATA 200670

QY      312 TCGAATCACAGTTTCAGTGTAGAGGGATTTGATATTTGGTCGACATTTTAAAGAGTTGT 371
DB      200671 TTTATATATATTTTAAATATAAATATATTTTAAATATAAATATATTTTAAATATA 200729

QY      372 TTTGTTTTTTTCCCAATCTGCATGGTTTTTCGTTCCGTTGAAACCAAAATTCACACCTTG 431
DB      200730 TATATAAATATATTTTAAATATAAATATATTTTAAATATAAATATATTTTAAATAT 200789

QY      432 TATAAACCGAATAGTAAATATACCTAGCGTACGCCAATACCAAAATATAAATTTAAACCTCA 491
DB      200850 ATTTTAAATATAAATAATAAATAATATATTTTAAATATAAATATAAATAATATAT 200909

QY      552 GAAATTTTAAATCGAGGATAATCAATATCCAACTCAACGATATCAAAAGCCTTAATAATAGA 611
DB      200910 ATATTTTAAATATAAATAATAAATAATATATTTTAAATATAAATAATAAATAAT 200969

QY      612 TCAATGAAATCAAAATAGTAAACATAGTAAATATACATTTGTTGTTAAACAGAAATAAT 671
DB      201029 ATATATTTTAAATATAAATAATAAATAATATATTTTAAATATAAATAATAAATAAT 201088

QY      672 ATACATTTAATAGTATGAAATAATGAATATATGAGATAAGAGCGGTATATGTTACAA 730
DB      201030 ATATATATTTTAAATATAAATAATAAATAATATATATTTTAAATATAAATAATAA 201088

RESULT 6
US-09-949-016-15852
; Sequence 15852, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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RESULT 7	
US-09-949-016-15853	
; Sequence 15853, Application US/09949016	
; Patent No. 6812339	
; GENERAL INFORMATION:	
; APPLICANT: VENTER, J. Craig et al.	
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED	
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF	
; FILE REFERENCE: CL001307	
; CURRENT APPLICATION NUMBER: US/09/949,016	
; CURRENT FILING DATE: 2000-04-14	
; PRIOR APPLICATION NUMBER: 60/241,755	
; PRIOR FILING DATE: 2000-10-20	
; PRIOR APPLICATION NUMBER: 60/237,768	
; PRIOR FILING DATE: 2000-10-03	
; PRIOR APPLICATION NUMBER: 60/231,498	
; PRIOR FILING DATE: 2000-09-08	
; NUMBER OF SEQ ID NOS: 207012	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO 15853	
; LENGTH: 205044	
; TYPE: DNA	
; ORGANISM: Human	
; FEATURE:	
; NAME/KEY: misc feature	
; LOCATION: (1)...(205044)	
; OTHER INFORMATION: n = A,T,C or G	
US-09-949-016-15853	
Query Match 3.4%; Score 69.8; DB 4; Length 205044;	
Best Local Similarity 46.3%; Pred. No. 0.00015;	
Matches 305; Conservative 0; Mismatches 347; Indels 7; Gaps 2;	
Qy	72 CATTCAAAAGGAAAAAATAATTTTGTATCTCTTAAAGTTTAACTTACATTTTC 131
Db	200437 CAAAAATAATCAAAATAATTTTAAATTTATATACATTTATAGTTTATCATCAAT 200496
Qy	132 CACACTTCAGTTGGTAGTATTAATTTATCTATTTTATCAAGTTTGGTTTACGAAAA 191
Db	200497 TTTATCAATATATTTAAATATAAATATATTTATATATATTTTAAATATAAATATAA 200556
Qy	192 ATGTATCTTTTCATATAAAAAATATATAGATCTTCAAGAAACTGAAATGGGTTTTCAC 251
Db	200557 ATATATTTATATATTTTAAATATAAATATAAATAATATATTTATATATTTTAA- 200615
Qy	252 TATTTTTCGTTTGACACTTCTGACTTATCAAAAGAGTTCAAAATAGAAAAATAGAA 311
Db	200616 -----TATAAATATATAAATAATATTTATATATATTTTAAATATAAATAATA 200670
Qy	312 TCGAATCACAGCTTTCAGTGAAGAGGATTTTGATATTTGGTCGACATTTTAAAGAGTTGT 371
Db	200671 TTTATATATATTTTAAATATAAATATAAATAATATTTATATATATTTTAAATA-TAAA 200729
Qy	372 TTTGTTTTTTTTTCCAACTCGCATGGTTTTCGTTCCGTTGAACCAAAATTCACACTTTG 431
Db	200730 TATATAAATAATTTTATATATATTTTAAATATAAATAATATAAATAATATTTATATAT 200789
Qy	432 TATAAACCGAATAGTAATATCTAGACGTAACCCATACCAAAATAAAATTTAAACTCA 491
Db	200790 TTTAAATAAATAATATAAATAATATATATTTTAAATATAAATAATATAAATAATATAT 200849
Qy	492 ATTACAAATTTGAATCTACACCATATCATGCGATATATATCAGCACTTAGAATAATCAAT 551
Db	200850 ATTTTAAATATAAATAATATAAATAATATATATTTTAAATATAAATAATATAAATAAT 200909
Qy	552 GAAATTTAATCGAGGATAATCAATATCCAACTCAACGATAATCAAAAGCCTTAATAATAGA 611
Db	200910 ATATTTTAAATATAAATAATATAAATAATATATATTTTAAATATAAATAATATAAATAAT 200969
Qy	612 TCAATGAAATCAAAATCAATAGTAAATATACATTTGATTTGGTTTAAACAGAAATAT 671
Db	200970 ATATATTTTAAATATAAATAATATAAATAATATATATTTTAAATATAAATAATATAAATAAT 201029

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RESULT 8	
US-09-949-016-12387	
; Sequence 12387, Application US/09949016	
; Patent No. 6812339	
; GENERAL INFORMATION:	
; APPLICANT: VENTER, J. Craig et al.	
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED	
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF	
; FILE REFERENCE: CL001307	
; CURRENT APPLICATION NUMBER: US/09/949,016	
; CURRENT FILING DATE: 2000-04-14	
; PRIOR APPLICATION NUMBER: 60/241,755	
; PRIOR FILING DATE: 2000-10-20	
; PRIOR APPLICATION NUMBER: 60/237,768	
; PRIOR FILING DATE: 2000-10-03	
; PRIOR APPLICATION NUMBER: 60/231,498	
; PRIOR FILING DATE: 2000-09-08	
; NUMBER OF SEQ ID NOS: 207012	
; SOFTWARE: FastSeq for Windows Version 4.0	
; SEQ ID NO 12387	
; LENGTH: 223471	
; TYPE: DNA	
; ORGANISM: Human	
; FEATURE:	
; NAME/KEY: misc feature	
; LOCATION: (1)...(223471)	
; OTHER INFORMATION: n = A,T,C or G	
US-09-949-016-12387	
Query Match 3.4%; Score 69.8; DB 4; Length 223471;	
Best Local Similarity 46.3%; Pred. No. 0.00015;	
Matches 305; Conservative 0; Mismatches 347; Indels 7; Gaps 2;	
Qy	72 CATTCAAAAGGAAAAAATAATTTTGTATCTCTTAAAGTTTAACTTACATTTTC 131
Db	170864 CAAAAATAATCAAAATAATATTTTAAATTTATATATTTTATCAATTTATAGTTTATCATCAAT 170923
Qy	132 CACACTTCAGTTGGTAGTATTAATTTATCTATTTTATCAAAAGTTTGGTTTACGAAAA 191
Db	170924 TTTATCAATATATTTTAAATATAAATATATTTTATATATATTTTAAATATAAATAATA 170983
Qy	192 ATGTATCTTTTCATATAAAAAATATATAGATCTTCAAGAAACTGAAATGGGTTTTCAC 251
Db	170984 ATATATTTTATATATATTTTAAATATAAATAATATAAATAATATATTTTATATATTTTAA- 171042
Qy	252 TATTTTTCGTTTGACACTTCTGACTTATCAAAAGAGTTTCAAAATAGAAAAATAGAA 311
Db	171043 -----TATAAATATAAATAATATATTTTATATATATTTTAAATATAAATAATA 171097
Qy	312 TCGAATCACAGCTTTCAGTGAAGAGGATTTTGATATTTGGTCGACATTTTAAAGAGTTGT 371
Db	171098 TTTATATATATTTTAAATATAAATAATATATAAATAATATTTATATATATTTTAAATA-TAAA 171156
Qy	372 TTTGTTTTTTTTTCCAACTCGCATGGTTTTCGTTCCGTTGAACCAAAATTCACACTTTG 431
Db	171157 TATAAATAAATAATTTTATATATATTTTAAATATAAATAATATAAATAATATATATAT 171216
Qy	432 TATAAACCGAATAGTAATATCTAGACGTAACCCATACCAAAATAAAATTTAAACTCA 491
Db	171217 TTTAAATAAATAATATAAATAATATATATTTTAAATATAAATAATATAAATAATATATAT 171276
Qy	492 ATTCAAAATTTGAATCTACACCATATCATGCGATATATATCAGCACTTAGAATAATCAAT 551
Db	171277 ATTTTAAATATAAATAATATAAATAATATATATTTTAAATATAAATAATATAAATAATAT 171336
Qy	552 GAAATTTAATCGAGGATAATCAATATCCAACTCAACGATAATCAAAAGCCTTAATAATAGA 611
Db	171337 ATATTTTAAATATAAATAATATAAATAATATATATTTTAAATATAAATAATATAAATAATAT 171396

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Qy      612 TCAATGAATCAATAACTAAACATAGTAATATATACATTGATTTGTGTTAAACAGAAATAT 671
Db      171397 ATATATTTTAAATATNAATATATATAAAATATATATATATTTTAAATATATAAATAT 171456
Qy      672 ATACATTATATAGTATGAAATATGAATATAAATGAGATAGAGCGGTATATGTTACAA 730
Db      171457 ATATATATTTTAAATATNAATATATATAAAATATATATATTTTAAATATATAAATAT 171515

RESULT 9
US-09-949-016-12724
; Sequence 12724, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12724
; LENGTH: 223471
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(223471)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12724

Query Match      3.4%; Score 69.8; DB 4; Length 223471;
Best Local Similarity 46.3%; Pred. No. 0.00015;
Matches 305; Conservative 0; Mismatches 347; Indels 7; Gaps 2;

Qy      72 CATTACAAAGGAAAAAATAATTTTGTATCTCTAAAGTTATAACTTACAATTTTC 131
Db      170864 CAAAAATAATCAANATATATTTAAATTTATATATATATATATATATATCAAT 170923
Qy      132 CACACTTCAGTTGGTAGTATTAATTTATCTATTTTATCAAAAGTTTGGTTTAGGAAA 191
Db      170924 TTTATCAATATATTTAAATATAAAATATATTTTAAATATAAATATATAAATA 171042
Qy      192 ATGATCTTTTCATATAAATAATATAGATCTTCAAGAACTGAATTTGGTTTCAAC 251
Db      170984 ATATATTTATATATATTTTAAATATAAATATATTTTAAATATAAATATATAA 171042
Qy      252 TATTTTATCGTTTGACACTACTTTGACTTATCAAAAGAGTTCAAAATAGAAAATAGAA 311
Db      171043 -----TATAAATATATAAATATATTTTATATATATTTTAAATATAAATATA 171097
Qy      312 TCGAATCACACGTTTCAGTGTAAAGAGGATTTGCATATTTGTCGACATTTTAAAGAGTTGT 371
Db      171098 TTTATATATATTTTAAATATAAATATATAAATATATAAATATATAAATATAAATA-TAAA 171156
Qy      372 TTTGTTTTTTTCCCAATCTGCATGTTTTCGTTCCGTTGAACCAAAATCAACACTTTG 431
Db      171157 TATATAAAATATATTTATATATATATTTTAAATATAAATATATAAATATATAAATATAT 171216
Qy      432 TATAAACCGAATAGTACTAGCATATATCATGCATATATATCATGCAACCTAGCAACCTCA 491
Db      171217 TTTAAATATAAATATAAATATATATTTTAAATATAAATATATAAATATATAAATATAT 171276
Qy      492 ATTCACAAATTTGAATCTACACCATATCATGCATATATATCATGCAACCTAGCAACCTCA 551
Db      171276 TTTAAATATAAATATAAATATATATTTTAAATATAAATATATAAATATATAAATATATATAT 171336
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Db      171277 ATTTTAAATATAAATATAAATATATATATTTTAAATATAAATATAAATATATAT 171336
Qy      552 GAAATTTAAATCGAGGATTAATCAATATCCAACTCAACGATTAATCAAAAGCCTTAATAATAGA 611
Db      171337 ATATTTTAAATATAAATATAAATATATATATTTTAAATATAAATATAAATATAT 171396
Qy      612 TCAATGAATCAATAACTAAACATAGTAATATACATTGATTTGTGTTAAACAGAAATAT 671
Db      171397 ATATATTTTAAATATNAATATATATAAAATATATATATTTTAAATATATAAATAT 171456
Qy      672 ATACATTATATAGTATGAAATATGAATATAAATGAGATAGAGCGGTATATGTTACAA 730
Db      171457 ATATATATTTTAAATATNAATATATATAAAATATATATATTTTAAATATAAATATATA 171515

RESULT 10
US-09-949-016-12725
; Sequence 12725, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12725
; LENGTH: 223471
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(223471)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12725

Query Match      3.4%; Score 69.8; DB 4; Length 223471;
Best Local Similarity 46.3%; Pred. No. 0.00015;
Matches 305; Conservative 0; Mismatches 347; Indels 7; Gaps 2;

Qy      72 CATTACAAAGGAAAAAATAATTTTGTATCTCTAAAGTTATAACTTACAATTTTC 131
Db      170864 CAAAAATAATCAANATATATTTAAATTTATATATATATATATATATATCAAT 170923
Qy      132 CACACTTCAGTTGGTAGTATTAATTTATCTATTTTATCAAAAGTTTGGTTTAGGAAA 191
Db      170924 TTTATCAATATATTTAAATATAAATATATTTTAAATATAAATATATAAATA 170983
Qy      192 ATGATCTTTTCATATAAATAATATAGATCTTCAAGAACTGAATTTGGTTTCAAC 251
Db      170984 ATATATTTATATATATTTTAAATATAAATATATTTTAAATATAAATATATAA 171042
Qy      252 TATTTTATCGTTTGACACTACTTTGACTTATCAAAAGAGTTCAAAATAGAAAATAGAA 311
Db      171043 -----TATAAATATATAAATATATTTTATATATATTTTAAATATAAATATA 171097
Qy      312 TCGAATCACACGTTTCAGTGTAAAGAGGATTTGCATATTTGTCGACATTTTAAAGAGTTGT 371
Db      171098 TTTATATATATTTTAAATATAAATATATAAATATATAAATATATAAATATAAATA-TAAA 171156
Qy      372 TTTGTTTTTTTCCCAATCTGCATGTTTTCGTTCCGTTGAACCAAAATCAACACTTTG 431
Db      171157 TATATAAAATATATTTATATATATATTTTAAATATAAATATATAAATATATAAATATAT 171216
Qy      432 TATAAACCGAATAGTACTAGCATATATCATGCATATATATCATGCAACCTAGCAACCTCA 491
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Db 171217 TTTAAATATAAATATATATATATTTTAAATATAAATATATATAAATATATAT 171276  
Qy 492 ATTCACAAATGAATCTACACCATATCATGCAATATATATACGCAACCTAGAAATCAAT 551  
Db 171277 ATTTTAAATATAAATATATATATATTTTAAATATAAATATATATAAATATAT 171336  
Qy 552 GAAATTTAATCGAGGATAATCAATATCAACTCAACGATATCAAAAGCCCTAAATAATAGA 611  
Db 171337 ATATTTTAAATATAAATATATAAATATATATATTTTAAATATAAATATATAAATAT 171396  
Qy 612 TCAATGAAATCAAATAACATAGTAATATACATTTGTTGTTTAAACAGAAATAT 671  
Db 171397 ATATATTTTAAATATAAATATATAAATATATATATTTTAAATATAAATATATAAAT 171456  
Qy 672 ATACATTAATAGTATGAAATATGAATATAATGAGATAGAGCGGTATATGTACAA 730  
Db 171457 ATATATATTTTAAATATAAATATATAAATATATATATTTTAAATATAAATATATAA 171515

## RESULT 11

US-09-949-016-16284  
; Sequence 16284, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16284  
; LENGTH: 29717  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(29717)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-16284

Query Match 3.4%; Score 68.8; DB 4; Length 29717;  
Best Local Similarity 47.0%; Pred. No. 0.00016;  
Matches 280; Conservative 0; Mismatches 312; Indels 4; Gaps 2;  
Qy 1436 TATATTGATGACAGATGTAAGTAATATATACATAAAATCATGTTTGTCTCAAGCATC 1495  
Db 15339 TATTTATATATATTTTATATATTTTATATATATTTATATATTTTATATATTTTATA 15398  
Qy 1496 TACGTTGAAATATATATAAGAGTTTGTGGTGAAGAAATATGATGAGAACTTCAT 1555  
Db 15399 TATATTTATATTTATATATATTTTATATATTTTATATATTTTATATATTTTATATA 15458  
Qy 1556 CTTTCATAATAGTGAACACTCTCTTCATACACCAAAAAAATTTGAAAAAATAG 1615  
Db 15459 TATTTTATATATTTTATATATATTTTATATATTTTATATATTTTATATATTTTATA 15518  
Qy 1616 TCAAACTCTCTTGTCCGATTAGGTTAGGTTGGACTCAGAAATCAAAATACGATTAGCAT 1675  
Db 15519 TATATATTTATATGATAT-ATTTTATATATTTTATATATTTTATATATTTTATATAT 15577  
Qy 1676 AACAAATTTTGGCATGGCAATTTGTCGACGGTAAAAATATACCAATAGAAACATAT 1735  
Db 15578 ATATTTTATATATTTATATACATATTTTATATATATTTTATATATTTTATATATACAT 15637

Qy 1736 TTTTGAAGTAGTTAAGATTATGATTGAAGAAATACATTTACGATAAGCATAAAAATTTTC 1795  
Db 15638 TTATATATATACATATTTTATATATATATATATATATTTTATATATATATATATATATAC 15697  
Qy 1796 TTTTGTCTTCTTGTGTTTGTCTTTTATAGAACATTTGATATGTAATGTTCTTTGTTT 1855  
Db 15698 ATATATTTTATTTATATATATTTTATATATTTTATATATTTTATATATTTTATATA 15757  
Qy 1856 TCACCAGTAGATGT---ACTATACACACATAGTAACATGGGTAGTTTATATAGAGAG 1912  
Db 15758 TTATTTTATATATTTTATATATTTTATATATTTTATATATTTTATATATATATTT 15817  
Qy 1913 AGATTTGATTTTTCGTATATTTCTTTTGTGAAATATAATGATGTAATAATTTATGTTT 1972  
Db 15818 ATATATTTTATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATATA 15877  
Qy 1973 ATTAATTTTGACAGATTTGTTTCACGTTGAGAGTTTAAATTTAGATTAACACACAAA 2028  
Db 15878 ATATATTTTATATATATTTTATATATTTTATATATTTTATATATTTTATATATGATA 15933

## RESULT 12

US-09-949-016-12423  
; Sequence 12423, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12423  
; LENGTH: 60376  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(60376)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12423

Query Match 3.4%; Score 68.8; DB 4; Length 60376;  
Best Local Similarity 47.0%; Pred. No. 0.00018;  
Matches 280; Conservative 0; Mismatches 312; Indels 4; Gaps 2;  
Qy 1436 TATATTGATGACAGATGTAAGTAATATATACATAAAATCATGTTTGTCTCAAGCATC 1495  
Db 47378 TATTTATATATATTTTATATATTTTATATATTTTATATATTTTATATATTTTATA 47437  
Qy 1496 TACGTTGAAATATATATAAGAGTTTGTGGTGAAGAAATATGATGAGAACTTCAT 1555  
Db 47438 TATATTTATATTTTATATATATTTTATATATTTTATATATTTTATATATTTTATA 47497  
Qy 1556 CTTTCATAATAGTGAACACTCTCTTCATACACCAAAAAAATTTGAAAAAATAG 1615  
Db 47498 TATTTATATATATTTTATATATATTTTATATATATTTTATATATATTTTATATATTT 47557  
Qy 1616 TCAAACTCTCTTGTCCGATTAGGTTAGGTTGGACTCAGAAATCAAAATACGATTAGCAT 1675  
Db 47558 TATATATTTATATGAT-ATTTTATATATTTTATATATTTTATATATTTTATATACAT 47616  
Qy 1676 AACAAATTTTGGCATGGCAATTTGTCGACGGTAAAAATATACCAATAGAAACATAT 1735  
Db 47617 ATATTTTATATATTTTATATACATATTTTATATATTTTATATATTTTATATATACAT 47676

Qy	1736	TTTTAGGAGTAGTTAAGATTATGATTGGAAGAAATACATTACGTAAGCATAAATTTTC	1795
Db	47677	TTATATATACATATTTATATATATACATATTTATATATATACACATATTTATATATAC	47736
Qy	1796	TTTTGCGTCTTTGGTTTTTGGTTTTATAGAACATTGGAATATGTACTTTTGGTTTTTTT	1855
Db	47737	ATATATTTATTTATATATATATTTATTTATATATTTATATATTTATATATATATATAT	47796
Qy	1856	TCACCAGTAGATATGT--ACTATACACACATATGATCATGCGGTAGTTTATATAGAGAG	1912
Db	47797	TTATATTTATATATATTTATATATTTATATATTTATATATTTATATATATATATTTT	47856
Qy	1913	AGATTTGGATTTTTCGTGATATTTCTTTTGTGAAATAAATATGTCGTAATAATTTATGTTT	1972
Db	47857	ATATATTTATTTATATATTTTACATATATTTATATTTATTTATTTATATTTATATTT	47916
Qy	1973	ATTAATTTGCAGATTTGTTCAGTTTGGAGAAGTTTAATTTAGATTTAAACAACAAA	2028
Db	47917	ATATATTTATATATATTTTATTTATTTATATATATTTGATTTTTCGTCACAAATGATA	47972

## RESULT 13

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US-09-949-016-15348
; Sequence 15348, Application US/09949016
; Patent No. 6612339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15348
; LENGTH: 134987
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15348

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D <sub>b</sub>	11574	TATAATTTTATATATATTATATATTATATATATTATATATTATATATTATATATTATATATA	11633
Q <sub>y</sub>	1738	TTAGGACGTAGTTAAAGATTATTCATTGAAGAATACTATTACCATAAGCATAAATTTTTCTT	1797
D <sub>b</sub>	11634	TTATATATATTTTATATATATATATATATTTATATATATATATATATATATATATATATAT	11693
Q <sub>y</sub>	1798	TTGGCTGTTCTTGCGTTTGGITCGITTTATAGAACATTCGAATATGTACTTTGTTTTTTTTC	1857
D <sub>b</sub>	11694	TATATTATATATATTTTATATATATAAATATATTGTATATATTATATATCTAATATATTATA	11753
Q <sub>y</sub>	1858	ACCACTAGATATGTACTATCACACATAAGTAACATGGTAGTTTATATAGAGAGAGATT	1917
D <sub>b</sub>	11754	TATATTATATATATTATATATTAATAATATATATTATATATTATATATATTTTTATATATA	11813
Q <sub>y</sub>	1918	TGATTTTTTCGTATATTTCTTTTGTTGGTAAPABATAATCGTAAAATTTTATGTTTTATTA	1977
D <sub>b</sub>	11814	TAATATGTATATATATAAATATATATAAAAACATATATAATATATATTTTATATTATATA	11873
Q <sub>y</sub>	1978	TTTGACAGATTTGTTCCAGTTTGAGAAGTTTAAATTTAGAT	2016
D <sub>b</sub>	11874	TATATTATATATATTATATATATTAAATATATATTTTATAT	11912

## RESULT 14

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US-09-949-016-15349
; Sequence 15349, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15349
; LENGTH: 134987
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15349

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Qy 1678 CAAATTTTGGCATGGCAATTAATGCTGCGAGTAAATATACCAATAGAAACATATTT 1737  
Db 11574 TATATATTTAT 11633  
Qy 1738 TTAGGAGTAGTAAAGATTAATGATTTGAAGAATACTATACGATAAGCATAAATTTTCTT 1797  
Db 11634 TTAT 11693  
Qy 1798 TTGCTGTTCTTGGTGTTCGTTTATAGAACAATTCGAATATGTAATTTTCTTTC 1857  
Db 11694 TAT 11753  
Qy 1858 ACCAGTAGATATGTAATATACACATAGTAAGTAAATGTTTATATAGAGAGATTT 1917  
Db 11754 TAT 11813  
Qy 1918 TGATTTTTCGTATATTTCTTTTGTGGAATAAATAATGCTGTAATAATTTTATTTAA 1977  
Db 11814 TAAATGTAATAAT 11873  
Qy 1978 TTTGACAGATTTGTTTCAGTTGAGAAAGTTTAAATTTAGAT 2016  
Db 11874 TAT 11912

Search completed: October 24, 2005, 00:56:20  
Job time : 350 secs

Db 11574 TATATATTTAT 11633  
Qy 1738 TTAGGAGTAGTAAAGATTAATGATTTGAAGAATACTATACGATAAGCATAAATTTTCTT 1797  
Db 11634 TTAT 11693  
Qy 1798 TTGCTGTTCTTGGTGTTCGTTTATAGAACAATTCGAATATGTAATTTTCTTTC 1857  
Db 11694 TAT 11753  
Qy 1858 ACCAGTAGATATGTAATATACACATAGTAAGTAAATGTTTATATAGAGAGATTT 1917  
Db 11754 TAT 11813  
Qy 1918 TGATTTTTCGTATATTTCTTTTGTGGAATAAATAATGCTGTAATAATTTTATTTAA 1977  
Db 11814 TAAATGTAATAAT 11873  
Qy 1978 TTTGACAGATTTGTTTCAGTTGAGAAAGTTTAAATTTAGAT 2016  
Db 11874 TAT 11912

RESULT 15  
US-09-949-016-15350  
; Sequence 15350, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15350  
; LENGTH: 134987  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15350

Query Match 3.3%; Score 67.8; DB 4; Length 134987;  
Best Local Similarity 46.2%; Pred. No. 0.00035;  
Matches 295; Conservative 0; Mismatches 342; Indels 2; Gaps 2;  
Qy 1380 CTACTAGGCTTCTCAATATTTTCCGAGAAATACAGAGGAAACAAAGTTAGTGATTATA 1439  
Db 11274 CTCCTTGGTTTAT 11333  
Qy 1440 TTGATGCGAGATGAGTAAGTAATATATA-CATAAATCATGTTTGTCTCAAGCATCTAC 1498  
Db 11334 TATTTATATAAATAAATAATAAATAATATATATATATATATATATATATATATATAT 11393  
Qy 1499 GTTGAATATATATAAGAGTTTCTTTTGGTGAATAAATAATGATGAGAGTTCATCTT 1558  
Db 11394 TAT 11453  
Qy 1559 TCATATAGTGAACAACTCTCTTTCATACCAAAAAAATTTGAAAAAATTAGTCA 1618  
Db 11454 TATTTAT 11513  
Qy 1619 AACTCTCTTTTGTCCGATTAAGTTAGGT-TTGGACTCAGAAATCAAAATACGATTAGCATAA 1677  
Db 11514 TAT 11573

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Perfect score: 2030  
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Gapop 10.0 , Gapext 1.0

Searched: 9772231 seqs, 4124568258 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2030	100.0	2042	22	US-10-643-676-2
3	1064	52.4	1064	9	US-09-938-842A-4152
4	1064	52.4	1064	11	US-09-938-842A-4152
5	90.2	4.4	8056	20	US-10-473-126-386
6	88.4	4.4	115218	21	US-10-278-698-255
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Query Match 100.0%; Score 2030; DB 22; Length 2030;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 1  
US-10-643-676-1  
; Sequence 1, Application US/10643676  
; Publication No. US20050176946A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry  
; APPLICANT: Nuccio, Michael  
; APPLICANT: Hsieh, Tsung-Fu  
; TITLE OF INVENTION: Constitutive promoter from Arabidopsis  
; FILE REFERENCE: A35897-PCT-USA-A (072667.0188)  
; CURRENT APPLICATION NUMBER: US/10/643,676  
; PRIOR FILING DATE: 2003-08-19  
; PRIOR APPLICATION NUMBER: PCT/EP02/02894  
; PRIOR FILING DATE: February 14, 2002  
; PRIOR APPLICATION NUMBER: 60/270,779  
; PRIOR FILING DATE: February 22, 2001  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2030  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-643-676-1

ALIGNMENTS

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Sequence 2128, App  
Sequence 1, Appli  
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Sequence 399, App  
Sequence 302, App  
Sequence 34, Appl  
Sequence 418, App  
Sequence 2121, App  
Sequence 155, App  
Sequence 301, App  
Sequence 6774, App  
Sequence 240, App  
Sequence 1, Appli  
Sequence 6381, App  
Sequence 10810, App  
Sequence 328, App  
Sequence 18, Appl  
Sequence 26, Appl  
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Sequence 55, Appl  
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Sequence 279, App  
Sequence 21, Appl  
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Sequence 36195, A  
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Sequence 36195, A

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Db 1861 AGTAGATATGCTACTATACACATACATACGATGAGTGGGTAGTTTATATAGAGAGATTGA 1920  
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Qy 1981 GACAGATTTGTTTCCGTTGAGAAAGTTTAAATTTAGATTTAAACCAACAAAAAG 2030  
Db 1981 GACAGATTTGTTTCCGTTGAGAAAGTTTAAATTTAGATTTAAACCAACAAAAAG 2030

RESULT 2  
US-10-643-676-2  
; Sequence 2, Application US/10643676  
; Publication No. US20050176946A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry  
; APPLICANT: Nuccio, Michael  
; APPLICANT: Heieh, Tzung-Fu  
; TITLE OF INVENTION: Constitutive promoter from Arabidopsis  
; FILE REFERENCE: A35897-PCT-USA-A (072697.0188)  
; CURRENT APPLICATION NUMBER: US/10/643,676



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US-09-938-842A-4152
; Sequence 4152, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4152
; LENGTH: 1064
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4152

Query Match 52.4%; Score 1064; DB 9; Length 1064;
Best Local Similarity 100.0%; Pred. No. 4.6e-184;
Matches 1064; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1747 GTTAAAGATTATGATTGAAGAAATACTATTACGATAAGCATAAAAAATTTCTTTTGCCTGTT 1806
Db 781 GTTAAAGATTATGATTGAAGAAATACTATTACGATAAGCATAAAAAATTTCTTTTGCCTGTT 840
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Db 841 TTGGTTTTTGTCTGTTTTATAGAAACATTGAATATGTAATTTTGTTTTTTTCACACAGTAGA 900
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## RESULT 4

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US-09-938-842A-4152
; Sequence 4152, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4152
; LENGTH: 1064
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4152
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Query Match 52.4%; Score 1064; DB 11; Length 1064;
Best Local Similarity 100.0%; Pred. No. 4.6e-184;
Matches 1064; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 967 GGTGACGTAACAAGACTTATTTCCGGTTGAATTTGGTTTAACTATTGAGATTGTGCTA 1026
Db 1 GGTGACGTAACAAGACTTATTTCCGGTTGAATTTGGTTTAACTATTGAGATTGTGCTA 60
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QY 1027 ACCGAAACAGAAACGGTTATGCGCCACGAGGCGGTAAACAGGAAGAGGG 1086
Db 61 ACCGAAACAGAAACGGTTATGCGCCACGAGGCGGTAAACAGGAAGAGGG 120
QY 1087 GATGCGAGAAATCGTAATTAACAGGAAATAAAGGGTGGTTTCAAGATAGTCTGCTA 1146
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QY 1147 TATGACGCGAAAGGTTCTTAAATTCAGAGAGACAATTAATAGTTTCGTTGTTGGA 1206
Db 181 TATGACGCGAAAGGTTCTTAAATTCAGAGAGACAATTAATAGTTTCGTTGTTGGA 240
QY 1207 GAAAGAGAGACAGATCAAAATACGAGAGAGATCTCTAAGAGATTTATCGTTTCAAGT 1266
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Db 421 GGTGTTTCAATATTTTTCCGAGAAATACGAGAGGACAAAGTTAGTGATTAATTTGATGC 480
QY 1447 AGAGTATCAAGTAAATATATATACATAAAATCATGTTTGTCTCAAGCATCTACGTTGAAAT 1506
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Db 541 ATATATAAGAAAGTTTTTTTTTGGTGAAAAAAATATGATGAGAAAGTTCAATCTTCAATA 600
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Db 661 TTGTCGCGATTAGTTAGTTGGACTCAGAACTCAAAATACGATTAGCATAAACAAATTTTT 720
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Db 841 TTGGTTTTTGTGCTTTTATAGAACTTGAATATGTAATCTTTGTTTTTTCACCAAGTAGA 900
QY 1867 TATGTAATATACACATAGTAAGTAACATGGTATGTTTATATAGAGAGAGATTTGATTTTTC 1926
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Db 961 GTATATTTCTTTTGTGAAATAAATATGCTGTAATAATTTTATGTTTATTAATTTGCACAGA 1020
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; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; FILE OF INVENTION: proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473.126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 386
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386
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Query Match 4.4%; Score 90.2; DB 20; Length 8056;  
Best Local Similarity 42.2%; Pred. No. 4e-06;  
Matches 840; Conservative 0; Mismatches 1128; Indels 23; Gaps 5;

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QY 87 AAAAAAATAATTTTTTGTATCTCTAAAGTTATAACTTACAAATTTTCCACACTTCAGTTGG 146
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QY 147 TAGTATTAAATTTATCTATTTTATCAAAAGTTGGTTTGGGAAATAATGATCTTTTCATA 206
Db 1873 TAATTAATAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTA 1814
QY 207 TAAAAATATATAGATCTTCAAGAAACTGAATTTGGGTTTTCACACTATTTTATCTTTGA 266
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QY 267 CACTACTTTGACTTATCAAAAGAGTTCCAAATAGAAAAATAGAAATCGAATCACACGTTT 326
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QY 327 CAGTGAAGAGGGATTGATTTGGTCGACATTTTAAAGAGTTGTTTGTGTTTTTTTCC 386
Db 1693 TAAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1634
QY 387 AATCTGATGTTTTCGTTGGAACCAAACTCAACACTTTCTGATATAAACCGAATAGT 446
Db 1633 ATTCATTTTATTTCAATTTTAAATAATATAAATAAATAAATAAATAAATAAATAAATA 1577
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QY 747 ACATTAACAATCCGATTTGGTGGCGCCATTTGTTGATATTTTGCACCTGATTTGATG 806
Db 1276 TATATTAATATAAATTAACATAACATTTTATTTTATTTTATTTTATTTTATTTAATA 1217
```



Qy	807	TGACTGCCAGCTGGCATAATATTTCCCTCCTCGATTAATGACGTTTGTATTACCTTTTACCTCTTCCCTCTCTGTT	866
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Qy	867	TCACGGTTAAATTCATTTTACTATTTTGTACCGCTGTCTTTTCACTCTTTTAAAGAAACCC	926
Db	1164	ATATATTAAATTTTAAATTTTCAAATATCAAAAAAATTTAAAAAACAATAATATATACAT	1105
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Qy	1167	TAAATTCAGAGAGACAATTAATCAGTTTCGTGTGTTGGAGAAAGAGAAACAGATCAA	1226
Db	864	AAAAATAAAAAAACAATTTTTTTTAAATAAAAAATTTTAAATAATCATTTATAAAATTTA	805
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Qy	1347	TTTTTAGTTCATGTGAATGAACCTCTGTTTTTATCTACTAGGGTTGTTTCAATATTTTTCCG	1406
Db	693	TTTTTATTTTATTTTATTTTTTTTTTTTTTTTTTAAATAAAATTTATTTTAA	634
Qy	1407	AGAATTACCAGAGAACAAAGTTAGTGAATATATTTGATGCAGAGTATGAAGTAATTTATAT	1466
Db	633	AAAAATTTTAAAAATTTATATAATATTTTTTTTATAAAATATTAATAATAATAATAATTT	574
Qy	1467	ACATAAATCATGTTTTGTTCTCAAGCATCTACGTTGAAATATATATAAGAAGTTTTTTTT	1526
Db	573	TAATAAACATTTATAATAATATATA-AAAATTTAAATTTTAAATAATAATTTAATAT	515
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Db	514	TATAAATATATAAATTTTAAATTTTTTTTATTTAAATATATTTTATTTTTTAAAAATTAAT	455
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Db	334	TTTTTTATTAATTTTTTTTTAAAAATAATTTTAAAAAATAAAAAATTTTTTTTATTA	275
Qy	1767	AATACTATACGATAAGCATAAAAATTTCTTTGCTGCTCTGTTGGTTTTGTCGTTTTATA	1826
Db	274	AAATAAAAT--TAAAAATTTTAAAAATTTTTTAAATTTTTTAAAAATTTTAAAAATTTTTTTA	217
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Db	216	AAAAATATAATAATAATTTAAATTTAAATTTTAAAAAATAATAATAAAAAATAAAAAA	157
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Query Match 3.7%; Score 75.4; DB 15; Length 8961;  
Best Local Similarity 45.1%; Pred. No. 0.0021;  
Matches 329; Conservative 0; Mismatches 391; Indels 9; Gaps 1;

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QY 90 AAAATAAATTTTGTCTTAAAGTTTAACTTCAAAATTTCCACACTTCAGTTGGTAG 149  
DB 5847 AAAATAAATTTTCCAAATTTAAAAAATAAATAAATAAATAAATAAATAAATAA 5788  
QY 150 TATTAATTTATCTATTTTATCAAAAGTTTGGTTTATAGGAAAAATCTATCTTTTCAATAA 209  
DB 5787 AAACATTTAAATTTATTAATTTCTTTTAAATAAATAAATAAATAAATAAATAAATAA 5728  
QY 210 AAAATATATAGATCTTCAAAAGAACTGAATTTGGTTTCAACTATTTTATCGTTTGACAC 269  
DB 5727 AAAACATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5668  
QY 270 TACTTTGACTTATCAAAAGAGTTCAAAATAGAAAAATAGAAATCAACACGTTTTCAG 329  
DB 5667 TAAAAACAACTTAAAAAATAAATTTATTAATAAATATCAATATAAATAAATAAATAA 5608  
QY 330 TGTAAGAGGGATTTGCATATTTGTCGACATTTTAAAGAGTTGTTTGTGTTTTTTTCCAA 389  
DB 5607 TTATTACGAATATAT-----ATAAATAAATAAATAAATAAATAAATAAATAAATAA 5557  
QY 390 CTGCAATGTTTTCGTTCCGTTGAACCAAAATTCACACCTTTGTATATAAACCAGTAAT 449  
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QY 450 ATACTAGAGTACGCAATACCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 509  
DB 5496 ATTATAAATAATCTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5437  
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DB 5436 CGAAATAATCTATTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5377  
QY 570 ATCAATATCCAACTCAACGATATCAAAAGCCTTAATAATAGATCAATGAAATCAAAATAC 629  
DB 5376 ATTAACATTTAAATCCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5317  
QY 630 TAAACATAGTATATACATTTGTTGTTAAACAGAAATAATATACATTTATTAATAGTAG 689  
DB 5316 TAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5257  
QY 690 AAAATATGAATATAATGAGATAAGAGCGGTATATGTTACAACTACAGATCACCACCA 749  
DB 5256 ATATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5197  
QY 750 ATTAACAAT 758  
DB 5196 TATATATAT 5188

RESULT 15  
US-10-981-277-34  
; Sequence 34, Application US/10981277  
; Publication No. US20050181389A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Cole  
; TITLE OF INVENTION: Compositions and Methods for Glioma Classification  
; FILE REFERENCE: 03-968-US  
; CURRENT APPLICATION NUMBER: US/10/981.277  
; CURRENT FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/516,817  
; PRIOR FILING DATE: 2003-11-03  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 34

LENGTH: 176096  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-981-277-34

Query Match 3.7%; Score 75; DB 22; Length 176096;  
Best Local Similarity 46.8%; Pred. No. 0.008;  
Matches 301; Conservative 0; Mismatches 340; Indels 2; Gaps 2;

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QY 106 TCCTAAAGCTTAACTTACAAATTTTCCACACTTCAGTTTGGTAGTATTAATTTATCTATT 165  
DB 166741 ATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 166800  
QY 166 TTTATCAAAAGTTTGGTTTATAGGAAAAATGATCTTTTCATATAAATAAATAAATAA 225  
DB 166801 ATATATAATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 166860  
QY 226 CAAGAACTCAATTTGGGTTTTCACACTATTTTATCGTTTGCACACTTCTGACTTATCAA 285  
DB 166861 ATATTATCAATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 166920  
QY 286 AAAGAGTTTCAAAATAGAAAAATAGAAATCGAAATCACACGTTTTCAGTTGTAAGGGATTTGA 345  
DB 166921 ATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 166980  
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DB 166981 TTATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 167040  
QY 406 TCCGTTGAACCAATTTCAACACTTTGTATAAACCGAAATAGTAATATCTAGACGTACGCC 465  
DB 167041 TATATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 167100  
QY 466 AATACCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 525  
DB 167101 AATATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 167160  
QY 526 TATATCAGCAACCTTGAATAATCAATGAAATTTAAATCGAGGTAATCAATATCCAACTCA 585  
DB 167161 ATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 167219  
QY 586 ACGATAATCAAAAGCCTTAATATAGATCAATGAAATCAAAATCAAAATCAAAATCAAAAT 645  
DB 167220 TTAATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 167279  
QY 646 CATTGATTTGTGTTAAACAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 688  
DB 167280 TATT-ATATGTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 167321

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Job time : 1660 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 23, 2005, 08:58:27 ; Search time 6674 Seconds  
(without alignment)  
11577.834 Million cell updates/sec

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Perfect score: 2030  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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C 2	663	32.7	679	8	AQ961293	AQ961293 LERPK31TR
C 3	426	21.0	426	9	CC796106	CC796106 SALK_0928
C 4	363.8	17.9	412	8	BZ597205	BZ597205 SALK_1004
C 5	311.8	15.4	396	9	CC796100	CC796100 SALK_0927
C 6	309.6	15.3	931	9	CL483650	CL483650 SAIL_384
C 7	256	12.6	223	8	BZ355348	BZ355348 SALK_1266
C 8	230	11.3	246	8	BH809771	BH809771 SALK_0056
C 9	156.6	7.7	749	8	BZ062372	BZ062372 l1e85b02.
C 10	147	7.2	713	8	BH439107	BH439107 BOHAK61TR
C 11	134.8	6.6	194	9	CR402809	CR402809 Arabidops
C 12	130	6.4	597	8	BH745927	BH745927 gz74a08.b
C 13	125.2	6.2	982	9	CL489509	CL489509 SAIL_525
C 14	119.6	5.9	786	8	BH425990	BH425990 BOGJF07TR
C 15	93.6	4.6	1592	9	CG750135	CG750135 P044-3-B0
C 16	93	4.6	207	1	AV832342	AV832342 AV832342
C 17	93	4.6	1101	9	CNS0039G	AL063921 Drosophil
C 18	92.8	4.6	507	1	AV825689	AV825689 AV825689
C 19	92.4	4.6	278	1	AJ609323	AJ609323 AJ609323
C 20	90.4	4.5	605	5	BP562932	BP562932 BP562932
C 21	89.2	4.4	1101	9	CNS000EVL	AL069706 Drosophil
C 22	88.4	4.4	495	7	T43150	T43150 6413 Lambda
C 23	87.8	4.3	636	5	BP561393	BP561393 BP561393
C 24	87.6	4.3	1896	9	CG753083	CG753083 P048-1-CO

25	87.4	4.3	463	7	T43139	T43139 6402 Lambda
C 26	87.2	4.3	1101	9	CNS000EVL	AL069706 Drosophil
C 27	87	4.3	516	7	H36351	H36351 14873 Lambda
C 28	86	4.2	1202	8	CC262481	CC262481 CH261-167
C 29	85.4	4.2	660	8	BH183498	BH183498 023.L-07-
C 30	85.4	4.2	660	9	CNS070NJ	AL620449 T3 end of
C 31	82.8	4.1	1190	9	CNS020N7	AL206908 Tetraodon
C 32	82.6	4.1	1101	9	CNS00KAE	AL077628 Drosophil
C 33	82.6	4.1	1225	9	CNS0161D	AL106171 Drosophil
C 34	82.4	4.1	515	7	CK119189	CK119189 213m19.p1
C 35	82.4	4.1	894	7	CF652281	CF652281 45-L02052
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C 38	81.4	4.0	2087	9	AG333887	AG333887 Mus muscu
C 39	81.2	4.0	1258	9	CL508886	CL508886 SAIL_804
C 40	81	4.0	1592	9	CG750135	CG750135 P044-3-D0
C 41	80.6	4.0	826	9	AG579614	AG579614 Mus muscu
C 42	80.6	4.0	1101	9	CNS0039G	AL063921 Drosophil
C 43	80.6	4.0	1391	9	CG754863	CG754863 P050-2-G0
C 44	80.4	4.0	722	7	CV481731	CV481731 AGENCOURT
C 45	80	3.9	782	7	CV484987	CV484987 AGENCOURT

ALIGNMENTS

RESULT 1  
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LOCUS LERPK31TF LERA Arabidopsis thaliana genomic clone LERPK31, genomic  
survey sequence.  
ACCESSION AQ961292  
VERSION AQ961292.1 GI:6788993  
KEYWORDS GSS  
SOURCE Arabidopsis thaliana (chale cress)  
ORGANISM Arabidopsis thaliana  
REFERENCE 1 (bases 1 to 679)  
AUTHORS Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T.,  
Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.  
TITLE Genomic survey sequencing of Landsberg erecta ecotype of  
Arabidopsis thaliana and identification of sequence-based  
polymorphisms  
JOURNAL Unpublished (2000)  
COMMENT Contact: Xiaoying Lin  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: at@tigr.org  
For additional information, see <http://www.tigr.org/tdb/at/at.html>  
Seq primer: TF  
Class: shotgun.

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ORIGIN

Query Match 33.0%; Score 669.4; DB 8; Length 679;  
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Matches 673; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1132 CGATAAGTCGTCTATATGACCGGAAGGGTTCTTAATTCAGAGACAATTAATCAG 1191  
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Db 619 TTTTCGTGTGTTTGGAGAAAGAAAGAACAGATCAAAATACGAGGAGAGATCTCTAAAGAGA 560  
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Db 559 TTTTATCGTTTCAAGTAACTCTTTATCAAACTCTTAATATATAACAAATCAAAACATGAA 500  
Qy 1312 CACGTGCTGTCCTGTTTCGATCTTAGATAGCAATTTTGTAGTTCATGTGAATGAATCTG 1371  
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Qy 1372 TTTTATTACTACTAGGTTGTTCAATATTTTTCGAGAAATACGAGGAAACAAAGTTAG 1431  
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Db 79 ATATTTTTCGATAGGTTAGGTTAGGTTTGGACTCAGATCAAAATACGATTA 20  
Qy 1792 TTTCTTTTTCGATAGGTTAGGTTTGGACTCAGATCAAAATACGATTA 1810  
Db 19 TTTCTTTTTCGATAGGTTAGGTTTGGACTCAGATCAAAATACGATTA 1

RESULT 2  
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DEFINITION LERFK31TR LERA Arabidopsis thaliana genomic clone LERFK31, genomic survey sequence.  
ACCESSION AQ961293  
VERSION AQ961293.1 GI:6788594  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (chale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 679)  
Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.  
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms  
JOURNAL Unpublished (2000)  
COMMENT Contact: Xiaoying Lin  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: at@tigr.org

For additional information, see <http://www.tigr.org/cdb/at/at.html>  
Seq primer: TR  
Class: shotgun.  
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ORIGIN

Query Match 32.7%; Score 663; DB 8; Length 679;  
Best Local Similarity 98.5%; Pred. No. 2.7e-104;  
Matches 669; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
Qy 939 TAACTATACGAAATCACATGCTTTCATGTGACGTAACAAGACTTATTTCCGGTTGAA 998  
Db 1 TAACTATACGAAATCACATGCTTTCATGTGACGTAACAAGACTTATTTCCGGTTGAA 60  
Qy 999 TTTGGTTTAACTTATTCAGATTGCTTAACCGAAACAGAAACGGTTATGACGCAACGA 1058  
Db 61 TTTGGTTTAACTTATTCAGATTGCTTAACCGAAACAGAAACGGTTATGACGCAACGA 120  
Qy 1059 GCGAAGAGGGTAAACAGAGAAAGAGGGATGCGAGAAATCGTAATTAACAAGAAAAA 1118  
Db 121 GCGAAGAGGGTAAACAGAGAAAGAGGGATGCGAGAAATCGTAATTAACAAGAAAAA 180  
Qy 1119 AAGGTGTTTTCAGGTAAGTCTGTATATGACGCGAAAGGGTTTCTTAATTCAGAGA 1178  
Db 181 AAGGTGTTTTCAGGTAAGTCTGTATATGACGCGAAAGGGTTTCTTAATTCAGAGA 240  
Qy 1179 GACAAATTAATCAGTTTCGTTGTTGGAGAAAGAAAGAAACAGATCAAAATACGAGGAGAG 1238  
Db 241 GACAAATTAATCAGTTTCGTTGTTGGAGAAAGAAAGAAACAGATCAAAATACGAGGAGAG 300  
Qy 1239 ATCTCTAAAGAGATTATTCGTTTCAAGTAAAGTCTCTTTTATCAAACTCTTAAATATAA 1298  
Db 301 ATCTCTAAAGAGATTATTCGTTTCAAGTAAAGTCTCTTATCAAACTCTTAAATATAA 360  
Qy 1299 ATCAAAACATGACACGTCGTTGTTTCGATCTAGATAGGATTTTCTAGTTTCATG 1358  
Db 361 ATCAAAACATGACACGTCGTTGTTTCGATCTAGATAGGATTTTCTAGTTTCATG 420  
Qy 1359 TGAATGAATCTGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1418  
Db 421 TGAATGAATCTGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480  
Qy 1419 GGAACAAAGTTAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1478  
Db 481 GGAACAAAGTTAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 540  
Qy 1479 TTTTGTCTCAAGCATCTAGTTTGAATATATATAGAAAGTTTTCGTTGTTTCGTTGTTTC 1538  
Db 541 TTTTGTCTCAAGCATCTAGTTTGAATATATATAGAAAGTTTTCGTTGTTTCGTTGTTTC 600  
Qy 1539 ATGTATGAGAAGTTTCACTTTTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1598  
Db 601 ATGTATGAGAAGTTTCACTTTTCAATTAATTAATTAATTAATTAATTAATTAATTAAT 660  
Qy 1599 ATTTGAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1617  
Db 661 ATTTGAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 679

RESULT 3  
LOCUS CC796106/c  
DEFINITION CC796106 426 bp DNA linear GSS 01-JUL-2003  
Arabidopsis thaliana genomic clone SALK\_092802.55.75.x, genomic



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Qy 1562 TAATAGTGAACAACTCTCTTTCATACCAAAAAAATTTGAAAAAAT-TAGTGAAA 1620
Db 241 TAATAGTGAACAACTCTCTTTCATACCAAAAAAATTTGAAAAAAGTGTGGGAAA 300
Qy 1621 CTCTCTTTGTCGATAGGTTAGGTTGGACTCAGAATCAAAATACGATTAGCATAACAA 1680
Db 301 CTCTCTTTGTCGATAGGTTAGGTTGGACTCAAAACCAAAATACTATTTCCTTAACCA 360
Qy 1681 ATTTTGGCATGCGAATATTATGTCGAGGTAAATATACCAATAGAAACA 1732
Db 361 ATTTTGGCATGCGAATATTATGTCGCGGAAAAATAAACCAATAAAAAACA 412

RESULT 5
CC796100 396 bp DNA linear GSS 01-JUL-2003
LOCUS SALK_092760.46.60.n Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_092760.46.60.n, genomic
survey sequence.
CC796100 1 GI:32391323
GSS.
Arabidopsis thaliana (Chale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 396)
REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
AUTHORS Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
The Salk Institute Genomic Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At4g20250.
Class: TDNA tagged.
FEATURES source
1..396
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_092760.46.60.n"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 15.4%; Score 311.8; DB 9; Length 396;
Best Local Similarity 98.4%; Pred. No. 9.1e-44;
Matches 350; Conservative 0; Mismatches 40; Indels 6; Gaps 1;

Qy 153 TAAATTTATCTATTTTATCAAAAGTTTGGTTTATAGAAAAATGTCATCTTTTCATATAAAA 212
Db 396 TAAATTTATCTATTTTATCAAAAGTTTGGTTTATAGAAAAATGTCATCTTTTCATATAAAA 337
Qy 213 ATATATAGATCTTCAAGAAACTGAATTTGGGTTTTCAACTATTTTATCGTTT-----GA 266
Db 336 ATATATAGATCTTCAAGAGAGCTGAATTTGGGTTTTCAGCTATTTTGTGCTTTTGACAGCT 277
Qy 267 CACTACTTTGACTTATCAAAAGAGTTTCAAAATAGAAAAATAGAATCGAATCACACAGTTT 326

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Db 276 GCTTGGGGCTTGTCAGAAAGNAGTTTCAGAAATAGAAAAATAGAAATCAGATCACAGTTT 217
Qy 327 CAGTGTAAGAGGATTTGATATATTGGTCGACATTTTAAAGAGTTGTTTGTGTTTTTTTCC 386
Db 216 CAGNGTAAGAGGATTTGATATATTGGTCGACATTTATAAAGAGGAGTTGTGTTGTTTTTCC 157
Qy 387 AATCTGCATCGTTTTCGTTCCGTTGCAACCAAAATTCACACACTTTGTATAAACCGAATAGT 446
Db 156 AATCTGCATCGTTTTCGTTCCGTTGCAACCAAAATTCACACACTTTGTATAAACCGAATAGT 97
Qy 447 AATATATCTAGACGTACGCCAATACCAAAAATAAAAATTTAAAACTCAATTCACAAATGAAT 506
Db 96 AATATATCTAGACGTACGCCAATACCAAAAATTTAAAACTCAATTCACAAATGTGAAT 37
Qy 507 CTCACCATATCATGTCATATATATATATATATATATATATATATATATATATATATATAT 542
Db 36 CTGCACCATATCATGTCATATATATATATATATATATATATATATATATATATATATATAT 1

RESULT 6
CL483650 931 bp DNA linear GSS 01-APR-2004
LOCUS SAIL_384_G12.v1 SAIL Collection Arabidopsis thaliana genomic clone
DEFINITION SAIL_384_G12.v1, genomic survey sequence.
ACCESSION CL483650
VERSION CL483650.1 GI:45958051
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 931)
REFERENCE Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
AUTHORS Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullig,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
A high-throughput Arabidopsis reverse genetics system
JOURNAL Plant Cell 14 (12), 2985-2994 (2002)
MEDLINE 22356987
PUBMED 12468722
COMMENT Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number CS817688; T-DNA left border flanking sequences of
SYNGENTA Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged.
FEATURES source
1..931
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
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/note="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"

ORIGIN
Query Match 15.3%; Score 309.6; DB 9; Length 931;
Best Local Similarity 65.3%; Pred. No. 2e-43;
Matches 521; Conservative 0; Mismatches 264; Indels 13; Gaps 4;

Qy 1121 GGGTGGTTTCAGGTAAGTCTGTCATATATACGCGAAAGGGTTTCTTAATTCAGAGAGA 1180
Db 137 GGGTGGTTCAGTAGTAATTTGGCTATATGACGCTAAAGGGTAACCTAAATTCGAAATGGA 196

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QY 1181 CAATTAATCATGTTCTGTCGTTGTTGGAGAAAGAAAGAACAGATCAATATACGAGGAGAT 1240
Db 1197 CTCCAACTCATATCGGAGCTTGACTAAAAGAAAGAACATATCGATCAAGGTAAAT 256
QY 1241 CTCTAAAGAGATTTATCGTTTCAAGTAAGTCTCTTTATCAAACTCTTTAATATAAACAAT 1300
Db 1257 CTGTAAAGAGATGATGCTCTATGCAAAATACCTTTTATCAAAAGTCTTTAATAGAAACAAT 316
QY 1301 CAAAACATGAACAGCTGTCGTCGTTTCGATTTCTAGATACGATTTTATGTTTCATG 1360
Db 1317 AAAAACATGAACAGCGGAGCATTTGGTGGCATATTTCTAAACAAATTTTATATCATG 376
QY 1361 AATGAACCTGTTTATTTACTACTAGGCTTGTTTCAATATTTTCCGAGAAATTTACCAGAG 1420
Db 1377 AATGAACCTGTTTACTACTACTAAACGTTGATCTTTTACGAGAAATTTACCAGAG 436
QY 1421 AACAAAGTTAGTATTAATTAATGATGACAGATGTAAGTAATTAATATATACATAAATCATGTT 1480
Db 1437 ACAA-----AGTTAAGCTTTATTTGGCGAGATACGAAAGAAATACTATCTTAAATCATGCC 491
QY 1481 TTGTTCTCAAGCATCTAGTTGAATATATATAAGAAAGTTTCTTTTCTGTAAGAAATAT 1540
Db 1492 GTGTTTATGGGACATCTAGCATGCAATATCTCTCAAGGCTTGTTTCGGGGATATAATAT 551
QY 1541 GTATGAGAGTTTCATCTTTTCAATAGTGAACAACTCTCTTCTATACCAAAAAAAT 1600
Db 1552 GATCACTAAGAGCGTCTTCAATATTAAGAAACAACTCTTTTCTATACCAAAAAAAT 611
QY 1601 TTGAAAAAATAATAGTGAACCTCTCTTTGTCGATTAAGTTAGTTGAGCTCAAGATCA 1660
Db 1612 TGGAGAAAAATTCGGGAACCTTTTTCCTGTTTGGAGAGGTTGGCCCAATTTCA 671
QY 1661 AATACGATAGCATACAAATTTTTCGATGCGCAATTAATTTGTCGAGGTAAATATA 1720
Db 1672 AA--GCCAATAACCTTACCTTTTTCGCTCGSAATCTATGCGCTTGGGGGANAATTA 729
QY 1721 CCAATAGAAACATATTTTGGAGTAGTTAAGATTAATGAAGAAATCTATTACGAT 1780
Db 1730 CCACTTGGACATTTTAAAGAGCTATTCAGATTTGATGGAANA-----TCTTTTCGG 786
QY 1781 AAGCATAAATTTCTTTGCTGTTCTTTGTTTTTGTCTGTTTATAGAACATGTAATG 1840
Db 1787 ATGGCATAACTTTCTTTTGGGACCTGGTTTTCGCGCTTTTA---AAACATGAANA 843
QY 1841 TACTTTGTTTTTTTCCACGATAGATATGATCTACTATACACATAGTAACATGGTAGT 1900
Db 1844 CACTTTGCTTTTTTTTCCCGCCCTTATTGCCATATCCACCCCGGAGGAGGTTT 903
QY 1901 TTATATAGAGAGATTT 1918
Db 1904 TTCAAAGGAATTTGTTTT 921

RESULT 7
BZ35348 323 bp DNA linear GSS 14-NOV-2002
LOCUS SALK_126660.22.95.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_126660.22.95.x, genomic
survey sequence.
ACCESSION BZ35348
VERSION BZ35348.1 GI:24946361
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
AUTHORS Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
```

JOURNAL  
COMMENT

Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of  
TDNA.

Class: TDNA tagged.

FEATURES  
source

Location/Qualifiers  
1..323  
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/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 12.6%; Score 256; DB 8; Length 323;  
Best Local Similarity 88.9%; Pred. No. 3.8e-34;  
Matches 288; Conservative 0; Mismatches 35; Indels 1; Gaps 1;  
QY 1690 CATGCCAATTAATGTCGAGGTAAATATACCAATAGAAACATATTTTAGGAGTAGTT 1749  
Db 1 CATGGAATTAATTCCTCGGTGTAATATATCCATTAGAAACTTCTTTGGGAGCATTT 60  
QY 1750 AGATTATGATTGAAGAAATACTATTACGATAGCATAAATTTCTTTGCTGTCCTG 1809  
Db 61 AAAATTATGATTGAAGAGATTCTTTTACGATAGGCTTGCAATTTCTTTGCTGCTCG 120  
QY 1810 GTTTTTCGTTTATAGAACATTCGAATATGATCTTTTGTGTTTTCACCACTAGATAT 1869  
Db 121 GTTTTTCGTTTATAGAACATTCGAATATGATCTTTTGTGTTTTCACCACTAGATAT 180  
QY 1870 GTACTATACACATAGTAACATCGGTAGTTTATATAGAGAGATTTGATTTTCGTA 1929  
Db 181 GTTCTATACCACTAAGTAACCTCGGTAGTTTATATAGAGAGATTTGATTTTCGTA 240  
QY 1930 TATTTCTTTGTTGAAATAAATATGTAATAATTTATTTATTTTACACATTT 1989  
Db 241 TATTTCTTTG-TGGAAATAAATATGTAATAATTTATTTTATTTTACACATTT 299  
QY 1990 GTTCAGTTGAGAGTTTAAATTA 2013  
Db 300 GTTCCCTCGGAAAGTTTAAATTA 323

RESULT 8  
BZ35348 246 bp DNA linear GSS 02-MAY-2002  
LOCUS SALK\_005656 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
thaliana genomic clone SALK\_005656, genomic survey sequence.

DEFINITION Arabidopsis thaliana (thale cress)  
ACCESSION BZ35348  
VERSION BZ35348.1 GI:20387588  
KEYWORDS Arabidopsis thaliana  
SOURCE Arabidopsis thaliana  
ORGANISM Arabidopsis thaliana  
REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
AUTHORS Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGnAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within an annotated exon of At4g20250.  
Class: TDNA tagged.  
Location/Qualifiers  
1. .246  
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/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)."

FEATURES  
source

1. .246  
/organism="Arabidopsis thaliana"  
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/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)."

ORIGIN

Query Match 11.3%; Score 230; DB 8; Length 246;  
Best Local Similarity 95.9%; Pred. No. 1.2e-29;  
Matches 236; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
Qy 855 TCCTCTTCTGTTTCCACCGTTAAATTCAAATTTTACTATTTGTACCGCTGCTTTTACCTTTT 914  
Db 1 TCCTCGTCTGTTTCCACCGTTAAATTCAAATTTTACTATTTGTACCGCTGCTTTTACCTTTT 60  
Qy 915 TTAAGAAACCCCAACCCGAAATCATATACCGAAATCATGTCTTCTATGTGACGT 974  
Db 61 TTAAGAAACCCCAACCCGAAATCATATACCGAAATCATGTCTTCTATGTGACGT 120  
Qy 975 AACAAAGCTTATTTTCCGGTTGAATTTGTTTAACTTATGAGATTGTGCTTAAACCGAAAA 1034  
Db 121 AACAAAGCTTATTTTCCGGTTGAATTTGTTTCACTTATGAGATTGTGCTTAAACCGAAAA 180  
Qy 1035 CAGAAACGGTTATGACGCCAACGAGGCAAGAGGGGTAAACGAGAAAGAGGGGATGGCAG 1094  
Db 181 CCGAAGCGGTTATGACGTCACCGGCAAGAGGGCAAAACGAGAAAGGGGATGGCGC 240  
Qy 1095 AAATCG 1100  
Db 241 AAATCG 246

RESULT 9  
BZ062372  
LOCUS 11e85b02.b1 B.oleracea002 Brassica oleracea genomic, genomic survey  
DEFINITION sequence.  
ACCESSION BZ062372  
VERSION BZ062372.1 GI:23672357  
KEYWORDS GSS.  
SOURCE Brassica oleracea  
ORGANISM Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 749)  
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,  
Naeh,W., Rabinowicz,P.D. and Wilson,R.K.  
Whole genome shotgun reads from Brassica oleracea  
Unpublished (2002)  
Contact: Richard K. Wilson

Genome Sequencing Center  
Washington University School of Medicine  
Email: [submissions@wustl.edu](mailto:submissions@wustl.edu)  
Plate: 11e85 row: b column: 02  
Seq primer: -21UPPOT forward  
Class: shotgun  
High quality sequence start: 21  
High quality sequence stop: 551.  
Location/Qualifiers  
1. .749

FEATURES  
source

/organism="Brassica oleracea"  
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/note="Vector: pOTw13; Whole genome shotgun library from  
flowering buds. DNA was purified from a crude nuclear  
prep using Brassica oleracea T0100DH3 buds provided by  
Thomas Osborn at the University of Wisconsin. Genomic  
DNA was provided by Pablo Rabinowicz (CSHL) and the  
shotgun library prepared at Washington University Genome  
Sequencing Center."

ORIGIN

Query Match 7.7%; Score 156.6; DB 8; Length 749;  
Best Local Similarity 66.8%; Pred. No. 4.7e-17;  
Matches 424; Conservative 0; Mismatches 159; Indels 52; Gaps 12;  
Qy 722 ATGTTCAACTACAGATCACCATCCCAATTAACAATCCGATTCGTCGGGGCCATTGTTT 781  
Db 32 ATTCATCCCTATAGATTACCATCTAATAATAACAATCCCATTCGATCGGGACCTACTTT 91  
Qy 782 CGATATTTGCCAACTGTGATTGATGACATGCCAGCTGGCATATTTTCCCTCTCGATTA 841  
Db 92 -GATCTTTGCCAACTCTGTTTGATGTACCGCAGCTGGCATATTTTCCATCTTAAATTA 150  
Qy 842 CGTTT-----TTACCCCTTTCTCTTCTTACCGTTAAATTCAAATTTTACTATTT 892  
Db 151 TGTTACCTTGGCTATCTCGGTTCTCTTCTGTTTGACAGTTATTCCTCAATATT-TAACTT 209  
Qy 893 GTACCGCTGCTTTTACCT-----TTTTTAAGAAAAACCCCAACCCGAAATCATTAAC 943  
Db 210 GTACTGCTGCTCTGACCCATTTCCGGTTATCGAAGAAAAATCAGAACTAAATAACACAG 269  
Qy 944 ATACCGAAATCACATGCTTCA-----TGGTGACGTAAACAAGACTTATTTTCGG 993  
Db 270 ATCCGAAACCGGTTTACATAAAACCATGGATGATGATTTGAAAAGTATTTTCGGT 329  
Qy 994 TTGAATTTGGTTTAAACCTATTGAGATTGTCTAACCGAAAAACGAAACGGTTATGACGCC 1053  
Db 330 TTAATGTTGCTTAATTGAGGAGATAACCGCGAAGAGACGACAGAAAAACGGTTAAGATGCC 389  
Qy 1054 AA-CGAGGCAAGAGGGGTAAACGAGAAAGAGGGGATGGCAGAAATCGTAATTAACRAGG 1112  
Db 390 AATTGAGGCAAGAGGGGTAA----AGAAGAGAGAGGGGGTCAATATCGTAAATTAAGAAG- 444  
Qy 1113 AAATAAAGGGTGGTTTTCAGATAAGTCTCTATATGACGCGAAAGGGTTTCTTAAATT 1172  
Db 445 AAAACAAGGGGTGATTTTGAAGAGAACCATATCTATATGACGTGAAGGGTT-----TT 497  
Qy 1173 CAGAGACACAATTAATCAGTTTTCGTGTGTTT-GGAGAAGAAGAGAAACAGATCAAAATACG 1231  
Db 498 CAGAGAACAATTAATCAGTTTTCGTGTGTTTCAAAGAAGAAGAGAAACAGATCAAAATACG 552  
Qy 1232 AGGAGAGATCTTAAAGAGATTTATCGTTTCAAGTAAGTCTCTTTATCAAACTCTTAAT- 1290  
Db 553 GACGGAGATCTCGAAAGAGATTTTATCATCTCAAGTAAGTTTCTATATCAAACTCGTGATG 612  
Qy 1291 --ATAACAATCAAAACATGAACACGCTCGTGCT 1323  
Db 613 AAATTAACAATCAAAACATGAATGTGTTTTT 647

RESULT 10







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Qy      838 ATTACGTTTTTACCGTTTCCTCTCTGTTTCCACCGTTAAATCAATTTTACTATTGTA 895
Db      137 ATTACGTTTTTACCGTTTCCTCTCTGTTTCCACCGTTAAATCAATTTTACTATTGTA 194

RESULT 12
BH745927/c
LOCUS   g274a08.b1 BoBuds01 Brassica oleracea genomic clone g274a08 5',
DEFINITION genomic survey sequence.
ACCESSION BH745927
VERSION   BH745927.1 GI:18880776
KEYWORDS
SOURCE    Brassica oleracea
ORGANISM  Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 597)
AUTHORS   Katari,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J.,
            Balija,V., Cummins,D.M., Katzenberger,F., King,L., Kirchoff,K.,
            Kuit,K., Miller,B., Muller,S., Nascimento,L., Preston,R.,
            Santos,L., Shah,R., Zutavern,T., Dedhia,N., Rabinowicz,P.D. and
            McCombie,W.R.
TITLE     Whole Genome Shotgun Reads from Brassica oleracea (2002b)
COMMENT   Unpublished (2002)
            Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mcombie@cshl.org
            Plate: g274 row: a column: 08
            Seq primer: -21UnivFwd
            Class: shotgun
            High quality sequence stop: 597.
FEATURES             source
            1..597
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            /clone="g274a08"
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            /notes="Vector: M13 for .x reads, pBluescript for .b and .g
            reads; Site 1: EcoRV; Whole genome shotgun library from
            flowering buds. DNA was purified from a crude nuclear prep
            using Brassica oleracea TO1000DH3 buds provided by Thomas
            Osborn at the University of Wisconsin. Genomic DNA
            provided by Pablo Rabinowicz (CSHL) and shotgun library
            prepared in McCombie Lab."
ORIGIN
Query Match          6.4%; Score 130; DB 8; Length 597;
Best Local Similarity 65.1%; Pred. No. 1.8e-12;
Matches 242; Conservative 0; Mismatches 120; Indels 10; Gaps 3;

Qy      553 AAATTTAATCGAGGATAATCAATATCCAACTCAACGATAATCAAAAGCCTTAATAATAGAT 612
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Qy      613 CA--ATGAAATCAATAACTAAACATAGTATATATACATTGATTTGTGTAAACAGATAAA 670
Db      482 TAACATCAATCGAATAATCAAAACAGATAATATAAAGGTCGTGATCTCTTAAACAGATAAA 423

Qy      671 TATACATTATAATAG-----TATGAAATATGAATATAATAGATAAGAGCGGTATAT 723
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Qy      904 TTTACACCTTTT 915
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DEFINITION SAIL_525_C07.v1, genomic survey sequence.
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VERSION   CL489509.1 GI:45971813
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ORGANISM  Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 982)
AUTHORS   Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
            Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
            Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kinmerly,B.,
            Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
TITLE     A high-throughput Arabidopsis reverse genetics system
JOURNAL   Plant Cell 14 (12), 2985-2994 (2002)
MEDLINE   22356987
PUBMED    12468722
COMMENT   Contact: Sessions A
            Applied Trait Genetics
            Syngenta Biotechnology Inc.
            3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
            Email: allen.sessions@syngenta.com
            ABRC Stock Number CS822250; T-DNA left border flanking sequences of
            Syngenta Arabidopsis Insertion Library (SAIL) lines are available
            through the Arabidopsis Biological Resource Center (ABRC).
            Sequences represent a pool of amplified genomic regions and not
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survey sequence.  
ACCESSION  
BH425990  
VERSION  
BH425990.1 GI:17611718  
KEYWORDS  
GSS.  
SOURCE  
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ORGANISM  
Brassica oleracea  
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
REFERENCE  
1 (bases 1 to 786)  
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.  
Whole genome shotgun sequencing of Brassica oleracea  
Unpublished (2001)  
Other\_GSSs: BOGJF07TF  
Contact: Chris Town  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TR  
Class: Sheared ends.  
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DB 139 GTTACACCTACAGATCACCATCCAGAAATTAACAATCCGATGGTGGGGCTCTACTTT-G 81  
QY 784 ATATTGCCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 843  
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DEFINITION  
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CG750135  
VERSION  
CG750135.1 GI:37971278  
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GSS.  
SOURCE  
Pristionchus pacificus  
ORGANISM  
Pristionchus pacificus  
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Neodiplogasteridae; Pristionchus.  
REFERENCE  
1 (bases 1 to 1592)  
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K.,  
Buntjer, J., van der Meulen, M. and Sommer, R.J.  
An integrated physical and genetic map of the nematode Pristionchus  
pacificus  
Mol. Genet. Genomics 269 (5), 715-722 (2003)  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
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QY 362 AAAGAGTTGTTTGTGTTTTTTTTTCCAACTCGCATGTTTTTTCGTCGTTGAACCAAT 421  
DB 955 ATAAAAATAATTTTNTATATATTTATTTATTTTNTAAAAATTAATAATAATAATA 896  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
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(without alignments)  
11237.757 Million cell updates/sec

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Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
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Post-processing: Listing first 1000 summaries

Database : GenEmbl.\*

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- 2: gb\_hcg.\*
- 3: gb\_in.\*
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- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pi.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_ats.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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132	22	1.1	133924	5	AC093712	AC093712 Canis fam	c 205	22	1.1	331039	3	AC116979	AC116979 Dictyoste
c 133	22	1.1	136804	9	AP000469	AP000469 Homo sapi	c 206	22	1.1	340080	9	AP001689	AP001689 Homo sapi
134	22	1.1	137858	2	AC151397	AC151397 Felis cat	c 207	22	1.1	349980	6	AX571760	AX571760 Sequence
c 135	22	1.1	139627	9	AL357117	AL357117 Human DNA	208	22	1.1	349980	132	HPA277788	HPA277788 Human pap
c 136	22	1.1	142506	2	CR678304	CR678304 Danio rer	209	21	1.0	374	6	CO407892	CO407892 Sequence
c 137	22	1.1	143137	5	AX004865	AX004865 Zebrafish	c 210	21	1.0	549	6	CO410381	CO410381 Sequence
c 138	22	1.1	143138	5	AL954181	AL954181 Zebrafish	c 211	21	1.0	555	8	AJ841026	AJ841026 Arabidops
139	22	1.1	146570	8	AC117076	AC117076 Dictyoste	c 212	21	1.0	622	6	CO427774	CO427774 Sequence
140	22	1.1	149634	9	AC113172	AC113172 Homo sapi	c 213	21	1.0	704	3	AY617813	AY617813 Sterkiell
141	22	1.1	149990	10	AC122803	AC122803 Mus muscu	c 214	21	1.0	1435	4	S74436	S74436 OIL-8-inter
142	22	1.1	151727	2	AC006894	AC006894 Caenorhab	215	21	1.0	1494	4	OAIL8	OAIL8 O.aries int
143	22	1.1	156221	2	AC134963	AC134963 Canis fam	c 216	21	1.0	1618	3	CEU55018	CEU55018 Caenorhabdi
144	22	1.1	156372	5	BX072531	BX072531 Zebrafish	c 217	21	1.0	2267	6	AR217142	AR217142 Sequence
c 145	22	1.1	157314	2	CR352289	CR352289 Danio rer	c 218	21	1.0	2267	6	AX206706	AX206706 Sequence
146	22	1.1	157847	10	AC122511	AC122511 Mus muscu	c 219	21	1.0	2267	10	MUSFISP12B	MUSFISP12B Mouse FISP-
147	22	1.1	159243	2	AC135660	AC135660 Rattus no	c 220	21	1.0	2334	6	BC006783	BC006783 Mus muscu
148	22	1.1	159647	5	EX897658	EX897658 Zebrafish	c 221	21	1.0	2338	6	E37595	E37595 Monoclonal
149	22	1.1	160557	2	CR759918	CR759918 Danio rer	c 222	21	1.0	2338	6	AR317175	AR317175 Sequence
150	22	1.1	162139	9	AC005682	AC005682 Homo sapi	c 223	21	1.0	2338	10	AB023068	AB023068 Rattus no
151	22	1.1	162797	2	AC023219	AC023219 Homo sapi	c 224	21	1.0	2350	6	BD242736	BD242736 Connectiv
152	22	1.1	168363	10	AL173917	AL173917 Mouse DNA	c 225	21	1.0	2350	6	AR194011	AR194011 Sequence
153	22	1.1	168910	5	CNS0989V	BX629357 Tetradon	c 226	21	1.0	2350	6	AR201286	AR201286 Sequence
154	22	1.1	169168	5	EX890629	BX890629 Zebrafish	c 227	21	1.0	2469	8	SCU02598	SCU02598 Saccharomyc
c 155	22	1.1	169604	2	BX640595	BX640595 Danio rer	c 228	21	1.0	2726	10	BC072503	BC072503 Rattus no
c 156	22	1.1	175345	2	AC022301	AC022301 Mus muscu	c 229	21	1.0	2957	8	YSCVPS16P	YSCVPS16P Rattus no
157	22	1.1	175527	2	AC107745	AC107745 Mus muscu	c 230	21	1.0	3041	5	AB005553	AB005553 Gallus ga
c 158	22	1.1	175936	2	SPNEU1908	AL449930 Streptoco	c 231	21	1.0	3065	8	SCNQP77	SCNQP77 X76245 S. cerevisia
c 159	22	1.1	177166	2	AC123979	AC123979 Papio anu	c 232	21	1.0	5307	6	AX348430	AX348430 Sequence
160	22	1.1	178534	2	AC027203	AC027203 Homo sapi	c 233	21	1.0	5307	6	AX348825	AX348825 Sequence
c 161	22	1.1	179724	9	AP003094	AP003094 Homo sapi	c 234	21	1.0	5725	3	AF482384	AF482384 Dictyoste
c 162	22	1.1	181230	5	BX296556	BX296556 Zebrafish	c 235	21	1.0	6204	6	AX346729	AX346729 Sequence
163	22	1.1	182871	3	AC117176	AC117176 Dictyoste	c 236	21	1.0	6207	6	AX251536	AX251536 Sequence
c 164	22	1.1	182871	3	AC117176	AC117176 Dictyoste	c 237	21	1.0	6821	2	AC017404	AC017404 Drosophila
c 165	22	1.1	183137	2	CR759797	CR759797 Danio rer	c 238	21	1.0	7644	8	TAU51303	TAU51303 Triticum ae

c 239	21	1.0	9357	6	AX251403	AX251403 Sequence	c 312	21	1.0	110191	3	AC087255	AC087255 Caenorhab
c 240	21	1.0	10425	6	C0607523	C0607523 Sequence	c 313	21	1.0	112512	2	AP003744	AP003744 Oryza sat
c 241	21	1.0	14095	6	AX345378	AX345378 Sequence	c 314	21	1.0	114505	8	F20B5	F20B5 Sequence
c 242	21	1.0	14644	9	HSBTKS4	HSBTKS4 Sequence	c 315	21	1.0	114534	5	BX294117	BX294117 Zebrafish
c 243	21	1.0	17070	8	AB001916	AB001916 Oryza sat	c 316	21	1.0	119238	8	AC137064	AC137064 Oryza sat
c 244	21	1.0	24942	3	CEK03D3	CEK03D3 Caenorhabdi	c 317	21	1.0	119745	8	AC141108	AC141108 Medicago
c 245	21	1.0	2520	3	AF099918	AF099918 Caenorhab	c 318	21	1.0	120743	8	AP004082	AP004082 Oryza sat
c 246	21	1.0	32847	3	AF025460	AF025460 Caenorhab	c 319	21	1.0	120926	2	AC133008	AC133008 Oryza sat
c 247	21	1.0	33038	3	CEY668	CEY668 Caenorhabdi	c 320	21	1.0	122479	3	CEY113G7A	CEY113G7A Caenorhab
c 248	21	1.0	33858	8	SCU44030	SCU44030 Saccharomyc	c 321	21	1.0	122715	10	AL845335	AL845335 Mouse DNA
c 249	21	1.0	36075	8	AF025468	AF025468 Caenorhab	c 322	21	1.0	122770	8	AC147007	AC147007 Medicago
c 250	21	1.0	36348	3	AC024765	AC024765 Caenorhab	c 323	21	1.0	123091	3	CEY87G2A	CEY87G2A Caenorhab
c 251	21	1.0	36865	3	AF098986	AF098986 Caenorhab	c 324	21	1.0	123623	3	AC151084	AC151084 Bos tauru
c 252	21	1.0	36865	3	AF098986	AF098986 Caenorhab	c 325	21	1.0	127883	10	AC114434	AC114434 Rattus no
c 253	21	1.0	43764	3	AF036699	AF036699 Caenorhab	c 326	21	1.0	127883	10	AP003118	AP003118 Oryza sat
c 254	21	1.0	44036	3	AF016672	AF016672 Caenorhab	c 327	21	1.0	129441	9	AL136170	AL136170 Human DNA
c 255	21	1.0	44364	3	AC091125	AC091125 Caenorhab	c 328	21	1.0	129461	2	CR677748	CR677748 Danio rer
c 256	21	1.0	44375	9	AC148448	AC148448 Pan trogl	c 329	21	1.0	131182	10	AC132259	AC132259 Mus muscu
c 257	21	1.0	44690	2	AC138022	AC138022 Botryllus	c 330	21	1.0	131741	8	AP004916	AP004916 Lotus cor
c 258	21	1.0	48891	8	AC082643	AC082643 Arabidops	c 331	21	1.0	132445	4	AY152826	AY152826 Felis cat
c 259	21	1.0	54441	3	AC115584	AC115584 Dictyoste	c 332	21	1.0	132906	2	AC145218	AC145218 Medicago
c 260	21	1.0	57538	3	AC115682	AC115682 Dictyoste	c 333	21	1.0	133197	2	AC146703	AC146703 Medicago
c 261	21	1.0	67374	9	CR394533	CR394533 Human DNA	c 334	21	1.0	133406	3	AF321227	AF321227 Tribolium
c 262	21	1.0	67392	9	AC034250	AC034250 Homo sapi	c 335	21	1.0	133575	8	CNS08C9N	CNS08C9N Oryza sat
c 263	21	1.0	68143	9	AC034250	AC034250 Homo sapi	c 336	21	1.0	134825	8	AC099325	AC099325 Oryza sat
c 264	21	1.0	68661	3	AC024805	AC024805 Caenorhab	c 337	21	1.0	136693	9	HS164F3	HS164F3 Homo sapi
c 265	21	1.0	69876	2	AC101484	AC101484 Mus muscu	c 338	21	1.0	137029	8	AC099040	AC099040 Human DNA
c 266	21	1.0	72586	10	AL732542	AL732542 Mouse DNA	c 339	21	1.0	138846	2	AC068478	AC068478 Homo sapi
c 267	21	1.0	73516	2	AC100369	AC100369 Mus muscu	c 340	21	1.0	139121	8	AP004846	AP004846 Oryza sat
c 268	21	1.0	73516	2	AC100369	AC100369 Mus muscu	c 341	21	1.0	139505	2	AC151072	AC151072 Bos tauru
c 269	21	1.0	75342	3	CEV47H9C	CEV47H9C Caenorhab	c 342	21	1.0	142414	8	AP004689	AP004689 Oryza sat
c 270	21	1.0	76213	2	AC108379	AC108379 Pan trogl	c 343	21	1.0	142898	2	CR387993	CR387993 Danio rer
c 271	21	1.0	7636	8	AB077822	AB077822 Arabidops	c 344	21	1.0	143163	9	HSBK21C21	HSBK21C21 Human DNA
c 272	21	1.0	77880	9	AC114766	AC114766 Homo sapi	c 345	21	1.0	143200	8	AP004380	AP004380 Oryza sat
c 273	21	1.0	78402	8	NCB16M17	NCB16M17 Neurospor	c 346	21	1.0	144596	8	AP004574	AP004574 Oryza sat
c 274	21	1.0	79318	3	AY171065S2	AY171065S2 Dictyoste	c 347	21	1.0	144781	9	HSJ585114	HSJ585114 Human DNA
c 275	21	1.0	80503	8	NC94C8	NC94C8 Neurospor	c 348	21	1.0	145146	2	AC126926	AC126926 Felis cat
c 276	21	1.0	81246	9	AX391354	AX391354 Arabidops	c 349	21	1.0	145975	2	AP004555	AP004555 Oryza sat
c 277	21	1.0	81677	8	AB025629	AB025629 Arabidops	c 350	21	1.0	146207	2	AP004555	AP004555 Oryza sat
c 278	21	1.0	81784	8	AC078893	AC078893 Oryza sat	c 351	21	1.0	146551	2	AC021604	AC021604 Homo sapi
c 279	21	1.0	81996	10	BX470237	BX470237 Mouse DNA	c 352	21	1.0	146570	3	AC117076	AC117076 Dictyoste
c 280	21	1.0	83373	5	BX284635	BX284635 Zebrafish	c 353	21	1.0	146824	2	AC118745	AC118745 Mus muscu
c 281	21	1.0	8400	8	AC010796	AC010796 Arabidops	c 354	21	1.0	148332	2	CR848023	CR848023 Danio rer
c 282	21	1.0	87885	8	AC007659	AC007659 Arabidops	c 355	21	1.0	148332	2	CR848023	CR848023 Danio rer
c 283	21	1.0	88356	8	AB0111479	AB0111479 Arabidops	c 356	21	1.0	148391	2	AC034174	AC034174 Homo sapi
c 284	21	1.0	89004	3	CEY69H2	CEY69H2 Caenorhabdi	c 357	21	1.0	149526	2	BX957346	BX957346 Danio rer
c 285	21	1.0	89249	3	AC103567	AC103567 Caenorhab	c 358	21	1.0	150663	2	AC074258	AC074258 Trypanoso
c 286	21	1.0	89479	8	AC006932	AC006932 Genomic s	c 359	21	1.0	151040	10	AC126040	AC126040 Mus muscu
c 287	21	1.0	95103	6	CQ754091	CQ754091 Sequence	c 360	21	1.0	151138	2	AC136727	AC136727 Mus muscu
c 288	21	1.0	96250	6	CQ754089	CQ754089 Sequence	c 361	21	1.0	151143	2	AC141740	AC141740 Apis mell
c 289	21	1.0	97021	2	AC138255	AC138255 Mus muscu	c 362	21	1.0	151143	2	AC146431	AC146431 Pan trogl
c 290	21	1.0	97789	8	AC004255	AC004255 Arabidops	c 363	21	1.0	151802	2	AP004363	AP004363 Oryza sat
c 291	21	1.0	97955	6	CQ754090	CQ754090 Sequence	c 364	21	1.0	152092	8	AP004363	AP004363 Oryza sat
c 292	21	1.0	99014	6	AX410782	AX410782 Sequence	c 365	21	1.0	154034	10	AL772336	AL772336 Mouse DNA
c 293	21	1.0	99014	6	HSU78027	HSU78027 Homo sapien	c 366	21	1.0	154216	2	AC120503	AC120503 Didelphis
c 294	21	1.0	99014	9	AL356436	AL356436 Homo sapi	c 367	21	1.0	154726	9	AL445923	AL445923 Human DNA
c 295	21	1.0	99163	2	AL356436	AL356436 Homo sapi	c 368	21	1.0	155232	2	AC149215	AC149215 Mus muscu
c 296	21	1.0	99659	10	AL732516	AL732516 Mouse DNA	c 369	21	1.0	155348	5	AL928820	AL928820 Zebrafish
c 297	21	1.0	101954	5	BX942844	BX942844 Zebrafish	c 370	21	1.0	156034	5	BX548043	BX548043 Zebrafish
c 298	21	1.0	103088	8	AC142395	AC142395 Medicago	c 371	21	1.0	156034	5	BX548043	BX548043 Zebrafish
c 299	21	1.0	103338	8	AC002294	AC002294 Arabidops	c 372	21	1.0	156419	8	AP002524	AP002524 Oryza sat
c 300	21	1.0	105726	10	AF037352	AF037352 Mus muscu	c 373	21	1.0	157348	2	AP002446	AP002446 Homo sapi
c 301	21	1.0	106159	4	AC124041	AC124041 Oryctolag	c 374	21	1.0	159336	9	AC020584	AC020584 Homo sapi
c 302	21	1.0	106527	2	AC148396	AC148396 Medicago	c 375	21	1.0	159375	9	AC020584	AC020584 Homo sapi
c 303	21	1.0	106527	2	AC148396	AC148396 Medicago	c 376	21	1.0	160487	9	AC087173	AC087173 Homo sapi
c 304	21	1.0	106935	3	AC087079	AC087079 Caenorhab	c 377	21	1.0	162784	2	AC114632	AC114632 Mus muscu
c 305	21	1.0	107284	8	AP005290	AP005290 Oryza sat	c 378	21	1.0	162911	9	AC073486	AC073486 Homo sapi
c 306	21	1.0	108582	8	AC011663	AC011663 Arabidops	c 379	21	1.0	163421	2	AL353792	AL353792 Homo sapi
c 307	21	1.0	110000	2	AC105495	AC105495 Rattus no	c 380	21	1.0	163634	2	AC141374	AC141374 Rattus no
c 308	21	1.0	110000	2	CEY102G3	CEY102G3 Continuation (2 of	c 381	21	1.0	163980	2	CR847967	CR847967 Danio rer
c 309	21	1.0	110000	2	CEY102G3	CEY102G3 Continuation (2 of	c 382	21	1.0	164147	8	AP005784	AP005784 Oryza sat
c 310	21	1.0	110000	2	CEY113B8	CEY113B8 Continuation (3 of	c 383	21	1.0	165361	10	AC125109	AC125109 Mus muscu
c 311	21	1.0	110000	8	CR380952	CR380952 Continuation (9 of	c 384	21	1.0	165458	2	AC009795	AC009795 Homo sapi

385	21	1.0	165504	2	AC026008	Homo sapi	458	21	1.0	200076	5	BX511258	BX511258	Zebrafish
386	21	1.0	165555	9	AL136962	Human DNA	459	21	1.0	201274	10	AC129335	AC129335	Mus muscu
387	21	1.0	165979	2	CR376741	Danio rer	c 460	21	1.0	201277	10	AC129183	AC129183	Mus muscu
388	21	1.0	166686	9	AC090450	Homo sapi	c 461	21	1.0	201746	2	AC006895	AC006895	Caenorhab
389	21	1.0	167117	9	AP001930	Homo sapi	462	21	1.0	201948	2	AP001026	AP001026	Homo sapi
390	21	1.0	167575	2	BX510344	Danio rer	463	21	1.0	202182	10	AC113304	AC113304	Mus muscu
391	21	1.0	168186	2	AC103403	Mus muscu	464	21	1.0	202346	10	AC121523	AC121523	Mus muscu
392	21	1.0	168192	2	AC103403	Mus muscu	c 465	21	1.0	202472	5	AL953892	AL953892	Zebrafish
393	21	1.0	168492	8	AC078839	Genomic S	c 466	21	1.0	202768	10	AC122849	AC122849	Mus muscu
394	21	1.0	168355	5	BX649631	Zebrafish	467	21	1.0	203127	5	BX322566	BX322566	Zebrafish
395	21	1.0	168366	2	AC069409	Homo sapi	468	21	1.0	203765	2	AC139635	AC139635	Gallus ga
396	21	1.0	169075	2	AC011940	Homo sapi	c 469	21	1.0	204859	2	AC019444	Danio rer	
397	21	1.0	169169	2	AC112837	Rattus no	c 470	21	1.0	205667	2	AC118762	Rattus no	
398	21	1.0	169364	3	CEY56A3A	Caenorhab	c 471	21	1.0	205625	2	AC004857	Danio rer	
399	21	1.0	169570	2	AC103058	Bos tauru	c 472	21	1.0	206525	2	AC1004857	Human chr	
400	21	1.0	170136	9	AC003082	Homo sapi	c 473	21	1.0	206722	9	CNS01DRU	Human chr	
401	21	1.0	170543	9	AC021012	Homo sapi	c 474	21	1.0	208817	9	AC145992	Pan trogl	
402	21	1.0	170544	9	CNS050TCC	Human chr	c 475	21	1.0	208909	5	BX004975	Zebrafish	
403	21	1.0	171058	5	BX323033	Zebrafish	c 476	21	1.0	209227	2	AC140380	Mus muscu	
404	21	1.0	172949	10	AC122323	Mus muscu	477	21	1.0	210202	2	AC124427	Mus muscu	
405	21	1.0	174133	8	AF083031	Guillard	478	21	1.0	210587	2	AC099626	Mus muscu	
406	21	1.0	174226	2	BX322792	Danio rer	479	21	1.0	210587	2	AC099626	Mus muscu	
407	21	1.0	174318	9	CNS01RGQ	Human chr	c 480	21	1.0	211860	2	AC141375	Rattus no	
408	21	1.0	174520	9	AC093432	Homo sapi	c 481	21	1.0	212842	9	AC102803	Homo sapi	
409	21	1.0	174752	10	AC132592	Mus muscu	c 482	21	1.0	213569	2	AC130899	Rattus no	
410	21	1.0	175097	9	AL354948	Human DNA	483	21	1.0	213729	2	AC150816	Callithr	
411	21	1.0	175320	9	AC009283	Homo sapi	c 484	21	1.0	214438	10	AC124546	Mus muscu	
412	21	1.0	175747	2	BX571952	Danio rer	c 485	21	1.0	216220	2	AC128490	Rattus no	
413	21	1.0	176782	2	AC103602	Mus muscu	c 486	21	1.0	216418	2	AC146604	Mus muscu	
414	21	1.0	177215	2	AC149715	Bos tauru	c 487	21	1.0	219525	2	AC142485	Rattus no	
415	21	1.0	177256	10	AC023972	Homo sapi	c 488	21	1.0	219621	2	CR391984	Danio rer	
416	21	1.0	177785	9	AP005431	Homo sapi	c 489	21	1.0	220563	2	AC128168	Rattus no	
417	21	1.0	178388	9	AC079630	Homo sapi	c 490	21	1.0	223342	2	AC106193	Rattus no	
418	21	1.0	178513	2	AC119832	Mus muscu	c 491	21	1.0	223392	10	AL670238	Mouse DNA	
419	21	1.0	178519	10	AC127256	Mus muscu	c 492	21	1.0	223844	10	AC126125	Rattus no	
420	21	1.0	178981	10	AL806511	Mouse DNA	c 493	21	1.0	223902	2	AC098627	Rattus no	
421	21	1.0	179144	9	AC026746	Homo sapi	494	21	1.0	224226	2	AC129414	Rattus no	
422	21	1.0	180018	2	AP001651	Homo sapi	c 495	21	1.0	224635	2	AC129871	Rattus no	
423	21	1.0	180055	9	AC063939	Homo sapi	c 496	21	1.0	224798	2	AC111617	Rattus no	
424	21	1.0	180511	2	AC139523	Rattus no	c 497	21	1.0	225314	2	BX004798	Mus muscu	
425	21	1.0	180992	9	AL136441	Human DNA	c 498	21	1.0	226361	2	AC094681	Rattus no	
426	21	1.0	182141	5	AL954645	Zebrafish	c 499	21	1.0	227833	2	AC128446	Rattus no	
427	21	1.0	182419	2	AC079321	Homo sapi	500	21	1.0	231559	2	AC111306	Rattus no	
428	21	1.0	182427	9	AL162390	Human DNA	501	21	1.0	235803	2	AC115551	Rattus no	
429	21	1.0	182801	2	AC132423	Mus muscu	c 502	21	1.0	237106	2	AC127762	Rattus no	
430	21	1.0	182906	2	AC131221	Rattus no	c 503	21	1.0	239246	2	AC102997	Rattus no	
431	21	1.0	183076	2	CR847536	Danio rer	c 504	21	1.0	240200	2	AC103040	Rattus no	
432	21	1.0	183086	9	AC097063	Homo sapi	c 505	21	1.0	240561	2	AC094485	Rattus no	
433	21	1.0	183472	3	AC132625	Mus muscu	506	21	1.0	242175	2	AC094969	Rattus no	
434	21	1.0	183648	3	AC117081	Dictyoste	507	21	1.0	242309	2	AC098167	Rattus no	
435	21	1.0	184111	2	AC110142	Rattus no	508	21	1.0	242577	2	AC121694	Rattus no	
436	21	1.0	184232	2	AC021535	Homo sapi	c 509	21	1.0	243489	2	AC096036	Rattus no	
437	21	1.0	184440	9	AP000919	Homo sapi	510	21	1.0	243508	2	AC078914	Mus muscu	
438	21	1.0	185369	10	AL671860	Mouse DNA	511	21	1.0	243510	5	BX005415	Zebrafish	
439	21	1.0	185558	10	AC121861	Mus muscu	c 512	21	1.0	244239	2	AC006880	Caenorhab	
440	21	1.0	186795	2	AC092884	Homo sapi	c 513	21	1.0	245375	2	AC094640	Rattus no	
441	21	1.0	187770	10	AL672054	Mouse DNA	c 514	21	1.0	245831	2	AC098069	Rattus no	
442	21	1.0	188661	2	AC147275	Pan trogl	515	21	1.0	246237	3	CEY39B6A	Caenorhab	
443	21	1.0	189572	2	AC119503	Rattus no	516	21	1.0	246867	2	AC111846	Rattus no	
444	21	1.0	189528	2	AC146318	Gallus ga	c 517	21	1.0	250029	3	AE014830	Plasmodiu	
445	21	1.0	190081	2	AC024737	Homo sapi	c 518	21	1.0	250713	3	AE014830	Plasmodiu	
446	21	1.0	190102	10	AC114640	Mus muscu	c 519	21	1.0	250713	3	AE014850	Mus muscu	
447	21	1.0	190620	2	AC101717	Mus muscu	520	21	1.0	250811	2	AC141896	Mus muscu	
448	21	1.0	191954	3	AC025726	Caenorhab	c 521	21	1.0	251096	10	AL956255	Mouse DNA	
449	21	1.0	192929	2	AC005505	Plasmodiu	522	21	1.0	253217	2	AC095502	Rattus no	
450	21	1.0	195072	2	CR382361	Danio rer	523	21	1.0	253322	2	AC110626	Rattus no	
451	21	1.0	195297	2	CR450803	Danio rer	524	21	1.0	254864	2	CR759802	Danio rer	
452	21	1.0	196023	10	AC122838	Mus muscu	c 525	21	1.0	255309	3	AE014832	Plasmodiu	
453	21	1.0	197762	10	AC119803	Mus muscu	c 526	21	1.0	258658	3	AE014832	Plasmodiu	
454	21	1.0	199521	2	AC079371	Mus muscu	c 527	21	1.0	260443	2	AC127131	Rattus no	
455	21	1.0	199745	5	AL805905	Zebrafish	c 528	21	1.0	260464	2	AC122960	Rattus no	
456	21	1.0	199814	3	CEY4703A	Caenorhab	529	21	1.0	261249	10	AC120856	Mus muscu	
457	21	1.0	199820	5	BX294113	Zebrafish	c 530	21	1.0	261341	2	AC122960	Mus muscu	
458	21	1.0	199820	5	BX294113	Zebrafish	c 530	21	1.0	261445	2	AC102580	Mus muscu	



531	21	1.0	263219	2	AC128778	AC128778 Rattus no	604	20	1.0	1645	6	AX509898	AX509898 Sequence
532	21	1.0	266344	9	AC005158	AC005158 Homo sapi	605	20	1.0	1666	5	CR761178	CR761178 Xenopus t
533	21	1.0	270693	2	AC097197	AC097197 Rattus no	606	20	1.0	1773	9	BC067243	BC067243 Homo sapi
534	21	1.0	270693	2	AC097197	AC097197 Rattus no	607	20	1.0	1789	5	YELXWNT	L07538 Frog wnt3A
535	21	1.0	278007	2	AC006799	AC006799 Caenorhab	608	20	1.0	1836	4	AF219241	AF219241 Loxodonta
536	21	1.0	278377	2	AC129839	AC129839 Rattus no	609	20	1.0	1905	5	CR523409	CR523409 Gallus ga
537	21	1.0	280335	2	AC105705	AC105705 Rattus no	610	20	1.0	2000	6	AX508509	AX508509 Sequence
538	21	1.0	280417	2	AC095158	AC095158 Rattus no	611	20	1.0	2037	6	CQ782415	CQ782415 Sequence
539	21	1.0	290066	2	AC129421	AC129421 Rattus no	612	20	1.0	2037	9	BD127120	BD127120 Primer fo
540	21	1.0	298015	2	AC006842	AC006842 Caenorhab	613	20	1.0	2037	9	AK074489	AK074489 Homo sapi
541	21	1.0	298820	2	AC006842	AC006842 Caenorhab	614	20	1.0	2057	10	AF060178	AF060178 Mus muscu
542	21	1.0	299820	2	AC006842	AC006842 Caenorhab	615	20	1.0	2146	8	YSCPEP4	M13358 Saccharomyc
543	21	1.0	300029	8	AE017105	AE017105 Oryza sat	616	20	1.0	2160	5	BC073416	BC073416 Xenopus l
544	21	1.0	300150	1	AP004594	AP004594 Cloanobac	617	20	1.0	2320	3	AK114986	AK114986 Ciona int
545	21	1.0	301450	1	AP003188	AP003188 Clostridi	618	20	1.0	2390	8	SCYPL154C	273510 S.cerevisia
546	21	1.0	302228	8	AE017070	AE017070 Oryza sat	619	20	1.0	2673	2	AK025438	AK025438 Homo sapi
547	21	1.0	304297	8	AE017088	AE017088 Oryza sat	620	20	1.0	2673	2	AK025438	AK025438 Homo sapi
548	21	1.0	305962	2	AC006746	AC006746 Caenorhab	621	20	1.0	2680	3	AF065437	AF065437 Aedes alb
549	21	1.0	305962	2	AC006746	AC006746 Caenorhab	622	20	1.0	2695	8	AK118006	AK118006 Arabidops
550	21	1.0	333321	3	AC116986	AC116986 Dictyoste	623	20	1.0	2715	8	AK069180	AK069180 Oryza sat
551	21	1.0	337720	2	AC121050	AC121050 Rattus no	624	20	1.0	2767	2	AC017589	AC017589 Drosophil
552	21	1.0	348034	3	CR382400	CR382400 Plasmodi	625	20	1.0	2853	6	AX833477	AX833477 Sequence
553	21	1.0	349907	1	BX571874	BX571874 Photorhab	626	20	1.0	2853	9	AK095249	AK095249 Homo sapi
554	21	1.0	349980	6	CQ870290	CQ870290 Sequence	627	20	1.0	3007	9	BC034979	BC034979 Homo sapi
555	21	1.0	349980	6	AX344554	AX344554 Sequence	628	20	1.0	3008	9	BC028710	BC028710 Homo sapi
556	21	1.0	349980	6	AX344554	AX344554 Sequence	629	20	1.0	3028	9	BC030784	BC030784 Homo sapi
557	20	1.0	20	20	AR360398	AR360398 Sequence	630	20	1.0	3073	9	HSM806062	BS537938 Homo sapi
558	20	1.0	20	20	AR360425	AR360425 Sequence	631	20	1.0	3100	6	CQ850945	CQ850945 Sequence
559	20	1.0	20	20	AX441509	AX441509 Sequence	632	20	1.0	3182	2	AC017715	AC017715 Drosophil
560	20	1.0	223	6	AX245416	AX245416 Sequence	633	20	1.0	3230	6	CQ588287	CQ588287 Sequence
561	20	1.0	240	6	AR553367	AR553367 Sequence	634	20	1.0	3266	9	HS20TOM5	AF126962 Homo sapi
562	20	1.0	421	11	BV188115	BV188115 sqm15689	635	20	1.0	3471	1	STYHIN	DI3690 S.abortus-e
563	20	1.0	425	6	AR351968	AR351968 Sequence	636	20	1.0	3497	5	BC084216	BC084216 Xenopus l
564	20	1.0	425	6	AX024980	AX024980 Sequence	637	20	1.0	3775	8	AX072083	AY072083 Arabidops
565	20	1.0	425	14	HPA010822	AJ010822 Human pap	638	20	1.0	3853	3	CQ608645	V00246 Transposabl
566	20	1.0	449	14	HPU124911	UI2499 Human papil	639	20	1.0	4089	3	DMTNFB	273509 S.cerevisia
567	20	1.0	511	11	BV008769	BV008769 MASC_STS1	640	20	1.0	4096	8	SCYPL153C	AX305892 Sequence
568	20	1.0	511	11	BV008770	BV008770 MASC_STS1	641	20	1.0	4128	6	AX305892	M70641 Mouse Fisp-
569	20	1.0	511	11	BV008773	BV008773 MASC_STS1	642	20	1.0	4128	10	MUSFTSP12A	AX345616 Sequence
570	20	1.0	537	11	BV008842	BV008842 MASC_STS1	643	20	1.0	4172	6	AX345616	L78750 Homo sapien
571	20	1.0	540	11	BV008777	BV008777 MASC_STS1	644	20	1.0	4743	9	HUM19DC93Z	AY591641 Mus muscu
572	20	1.0	541	11	BV008777	BV008777 MASC_STS1	645	20	1.0	4781	10	AX591641	AX300905 Sequence
573	20	1.0	547	11	BV008768	BV008768 MASC_STS1	646	20	1.0	5158	6	AX300905	AC014042 Drosophil
574	20	1.0	552	11	BV008377	BV008377 MASC_STS1	647	20	1.0	5345	2	AC014042	AX251238 Sequence
575	20	1.0	554	11	BV008377	BV008377 MASC_STS1	648	20	1.0	5571	6	AX251238	AX251941 Sequence
576	20	1.0	554	11	BV008767	BV008767 MASC_STS1	649	20	1.0	5571	6	AX251941	AX344433 Sequence
577	20	1.0	597	6	AX187052	AX187052 Sequence	650	20	1.0	5571	6	AX344433	AX344433 Sequence
578	20	1.0	621	6	CQ741526	CQ741526 Sequence	651	20	1.0	5571	6	AX344433	AX344433 Sequence
579	20	1.0	664	6	AX320465	AX320465 Sequence	652	20	1.0	5571	6	AX344433	AX344433 Sequence
580	20	1.0	692	1	STYHIN1	M12292 S.typhimuri	653	20	1.0	5608	9	HSM809103	AX323784 Sequence
581	20	1.0	700	8	ATH527660	AJ527660 Arabidops	654	20	1.0	5986	6	AX323784	AF096095 Arabidops
582	20	1.0	712	8	AY027408	AY027408 Arabidops	655	20	1.0	6081	8	AF096095	AF096095 Arabidops
583	20	1.0	746	11	G55787	G55787 SHGC-101003	656	20	1.0	6458	6	BD223811	BD223811 Novel met
584	20	1.0	783	6	CQ428063	CQ428063 Sequence	657	20	1.0	6656	6	AX453099	AX453099 Sequence
585	20	1.0	791	8	AK105197	AK105197 Oryza sat	658	20	1.0	6656	6	AX281211	AX356484 Sequence
586	20	1.0	801	8	AK104930	AK104930 Oryza sat	659	20	1.0	6656	6	AX356484	AB014605 Homo sapi
587	20	1.0	858	11	BV054686	BV054686 S212P6620	660	20	1.0	6795	9	AB014605	AX346666 Sequence
588	20	1.0	898	8	AC065736	AC065736 Oryza sat	661	20	1.0	8029	1	ECFDPKX	X14436 Escherichia
589	20	1.0	944	9	BC008823	BC008823 Homo sapi	662	20	1.0	8029	1	AY395706	AX395706 Human pap
590	20	1.0	968	6	AX300906	AX300906 Sequence	663	20	1.0	8092	14	AX395706	AX281525 Sequence
591	20	1.0	976	8	BT012903	BT012903 Lycopersi	664	20	1.0	8662	6	AX281525	AC017666 Drosophil
592	20	1.0	1002	8	AF402570	AF402570 Maesa jap	665	20	1.0	10105	2	AC017666	X72695 T.maritima
593	20	1.0	1094	1	STYFLGH2C	J01801 Salmonella	666	20	1.0	10120	2	TMRPO	CQ607523 Sequence
594	20	1.0	1094	6	AR124196	AR124196 Sequence	667	20	1.0	10425	6	CQ607523	AC119287 Caenorhab
595	20	1.0	1149	1	STHINZ	V01370 Salmonella	668	20	1.0	10762	3	AC119287	AX345366 Sequence
596	20	1.0	1205	11	BV177783	BV177783 sqm96694	669	20	1.0	10891	6	AX345366	AE005523 Escherich
597	20	1.0	1312	5	BX932433	BX932433 Gallus ga	670	20	1.0	11293	1	AE005523	AE015305 Shigella
598	20	1.0	1320	1	AF494421	AF494421 Lactobaci	671	20	1.0	11490	1	AE015305	AE002129 Ureaplaem
599	20	1.0	1363	5	BX929958	BX929958 Gallus ga	672	20	1.0	12511	1	AE002129	CQ806991 Sequence
600	20	1.0	1560	6	AX510083	AX510083 Sequence	673	20	1.0	12610	6	CQ806991	CQ807265 Sequence
601	20	1.0	1600	8	AK104695	AK104695 Oryza sat	674	20	1.0	12610	6	CQ807265	U80841 Caenorhabd
602	20	1.0	1602	3	AY204183	AY204183 Caenorhab	675	20	1.0	14687	3	U80841	AX346416 Sequence
603	20	1.0	1637	8	AK067442	AK067442 Oryza sat	676	20	1.0	15399	6	AX346416	

c 677	20	1.0	16918	6	AX346519	AX346519 Sequence
c 678	20	1.0	20420	1	AS001724	AS001724 Thermotog
c 679	20	1.0	20513	1	AE008826	AE008826 Salmonell
c 680	20	1.0	21123	2	AC012820	AC012820 Drosophil
c 681	20	1.0	21260	3	AC024813	AC024813 Caenorhab
c 682	20	1.0	21560	6	C0584033	C0584033 Sequence
c 683	20	1.0	23260	3	AF099927	AF099927 Caenorhab
c 684	20	1.0	23058	3	AF099927	AF099927 Caenorhab
c 685	20	1.0	23764	3	AC006723	AC006723 Caenorhab
c 686	20	1.0	24686	3	CEY43F11A	CEY43F11A Caenorhab
c 687	20	1.0	25426	3	AC006747	AC006747 Caenorhab
c 688	20	1.0	25568	3	AC116955	AC116955 Dictyoste
c 689	20	1.0	25851	3	AF025466	AF025466 Caenorhab
c 690	20	1.0	26547	3	U70844	U70844 Caenorhabdi
c 691	20	1.0	26874	3	CEB10255	CEB10255 Caenorhabdi
c 692	20	1.0	29546	3	AF003390	AF003390 Caenorhab
c 693	20	1.0	29976	3	U50197	U50197 Caenorhabdi
c 694	20	1.0	30305	3	AF100305	AF100305 Caenorhab
c 695	20	1.0	31876	3	AF078783	AF078783 Caenorhab
c 696	20	1.0	32323	2	AC022228	AC022228 Mus muscu
c 697	20	1.0	32940	3	AF022972	AF022972 Caenorhab
c 698	20	1.0	33000	3	CEK11H3	CEK11H3 Caenorhabdi
c 699	20	1.0	33796	3	U56964	U56964 Caenorhabdi
c 700	20	1.0	35121	2	CEC43A10	CEC43A10 Caenorhab
c 701	20	1.0	35137	8	AC007196	AC007196 Arabidops
c 702	20	1.0	36096	6	AX059472	AX059472 Sequence
c 703	20	1.0	36494	3	CEP59D12	CEP59D12 Caenorhabdi
c 704	20	1.0	36582	3	AF036689	AF036689 Caenorhab
c 705	20	1.0	36888	3	U93378	U93378 Caenorhabdi
c 706	20	1.0	37034	3	CBRGA7D14	CBRGA7D14 Caenorhab
c 707	20	1.0	37059	3	CEK02E2	CEK02E2 Caenorhabdi
c 708	20	1.0	37521	2	AC149354	AC149354 Phakopos
c 709	20	1.0	38556	3	CEY43P8A	CEY43P8A Caenorhab
c 710	20	1.0	39121	3	CBF09C6	CBF09C6 Caenorhabdi
c 711	20	1.0	39236	3	CEP59A1	CEP59A1 Caenorhabdi
c 712	20	1.0	39271	3	CEP52G2	CEP52G2 Caenorhabdi
c 713	20	1.0	39348	9	AL354670	AL354670 Human DNA
c 714	20	1.0	39555	3	CEZK262	CEZK262 Caenorhabdi
c 715	20	1.0	39634	2	AC145715	AC145715 Homo sapi
c 716	20	1.0	39974	3	AF099921	AF099921 Caenorhab
c 717	20	1.0	40466	3	U58749	U58749 Caenorhabdi
c 718	20	1.0	40766	3	AF101305	AF101305 Caenorhab
c 719	20	1.0	41627	3	U41528	U41528 Caenorhabdi
c 720	20	1.0	41778	3	AF036700	AF036700 Caenorhab
c 721	20	1.0	42703	3	CSC09P9	CSC09P9 Caenorhabdi
c 722	20	1.0	42886	9	AC016762	AC016762 Homo sapi
c 723	20	1.0	43884	3	CEC25F9	CEC25F9 Caenorhabdi
c 724	20	1.0	45232	3	AF100657	AF100657 Caenorhab
c 725	20	1.0	45510	3	CSC32A3	CSC32A3 Caenorhabdi
c 726	20	1.0	45635	3	AF026205	AF026205 Caenorhab
c 727	20	1.0	46387	2	U82212	U82212 Homo sapien
c 728	20	1.0	47328	6	AX059532	AX059532 Sequence
c 729	20	1.0	47440	9	U73509	U73509 Homo sapien
c 730	20	1.0	48397	2	AC015399	AC015399 Drosophil
c 731	20	1.0	51015	9	AL732292	AL732292 Human DNA
c 732	20	1.0	52139	3	AC006790	AC006790 Caenorhab
c 733	20	1.0	52684	2	AC014796	AC014796 Drosophil
c 734	20	1.0	54475	3	AC024812	AC024812 Caenorhab
c 735	20	1.0	55786	8	SCLACHXVI	SCLACHXVI S.cerevisia
c 736	20	1.0	55965	3	AC104653	AC104653 Homo sapi
c 737	20	1.0	56012	2	AC100094	AC100094 Mus muscu
c 738	20	1.0	57795	9	AC004219	AC004219 Homo sapi
c 739	20	1.0	58200	2	AC091188	AC091188 Homo sapi
c 740	20	1.0	58804	8	CEB38949	CEB38949 Continuation (6 of
c 741	20	1.0	59533	3	AC084450	AC084450 Caenorhab
c 742	20	1.0	59577	9	AL589796	AL589796 Human DNA
c 743	20	1.0	61910	2	AC101194	AC101194 Mus muscu
c 744	20	1.0	63680	2	AC101117	AC101117 Mus muscu
c 745	20	1.0	63747	3	AC025727	AC025727 Caenorhab
c 746	20	1.0	64093	3	AC025727	AC025727 Caenorhab
c 747	20	1.0	64136	8	AB024031	AB024031 Arabidops
c 748	20	1.0	64670	2	AC136714	AC136714 Continuation (4 of
c 749	20	1.0	66253	2	AC023372	AC023372 Homo sapi

c 750	20	1.0	66253	2	AC023372	AC023372 Homo sapi
c 751	20	1.0	66796	2	AC017435	AC017435 Drosophil
c 752	20	1.0	67552	8	AP006677	AP006677 Locust cor
c 753	20	1.0	67706	3	AC073517	AC073517 Homo sapi
c 754	20	1.0	67970	3	PFMAL1P3	PFMAL1P3 Plasmodiu
c 755	20	1.0	68301	9	AL158065	AL158065 Human DNA
c 756	20	1.0	69381	9	HSJ301L19	HSJ301L19 Human DNA
c 757	20	1.0	69692	8	AC121763	AC121763 Genomic s
c 758	20	1.0	70145	2	AC101291	AC101291 Mus muscu
c 759	20	1.0	70704	8	NCB8L21	NCB8L21 Neurospor
c 760	20	1.0	72175	2	AC101418	AC101418 Mus muscu
c 761	20	1.0	72175	2	AC101418	AC101418 Mus muscu
c 762	20	1.0	72412	2	AC101594	AC101594 Mus muscu
c 763	20	1.0	72412	2	AC101594	AC101594 Mus muscu
c 764	20	1.0	73101	8	AP006122	AP006122 Locust cor
c 765	20	1.0	75073	3	CEY48A6B	CEY48A6B Caenorhab
c 766	20	1.0	75289	8	AB023046	AB023046 Arabidops
c 767	20	1.0	78172	8	AB010070	AB010070 Arabidops
c 768	20	1.0	82033	8	AB011476	AB011476 Arabidops
c 769	20	1.0	83024	9	AC000389	AC000389 Genomic s
c 770	20	1.0	83601	9	AC079172	AC079172 Homo sapi
c 771	20	1.0	85214	8	AC005396	AC005396 Arabidops
c 772	20	1.0	85812	2	AC040952	AC040952 Homo sapi
c 773	20	1.0	88839	3	AC084447	AC084447 Caenorhab
c 774	20	1.0	89840	8	AC004705	AC004705 Arabidops
c 775	20	1.0	90335	8	ATT5N23	ATT5N23 Arabidops
c 776	20	1.0	90901	9	HSJ417120	HSJ417120 Human DNA
c 777	20	1.0	90963	2	AC079626	AC079626 Mus muscu
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## ALIGNMENTS

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AX548023 2030 bp DNA linear PAT 26-NOV-2002
LOCUS Sequence 1 from Patent WO2068665.
DEFINITION AX548023
ACCESSION AX548023
VERSION AX548023.1 GI:25813131
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SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids_II; Brassicales; Brassicaceae; Arabidopses.
REFERENCE 1
AUTHORS Thomas, T., Nuccio, M. and Hsieh, T.F.
TITLE Constitutive promoter from arabidopsis
JOURNAL Patent: WO 0206865-A 1 06-SEP-2002;
Rbioio (PR)
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## ORIGIN

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Query Match 100.0%; Score 2030; DB 6; Length 2030;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
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Thomas, T., Nuccio, M. and Heieh, T.F.			
Constitutive promoter from arabidopsis			
Patent: WO 02068665-A 2 06-SEP-2002;			
Rbio (FR)			

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AL022224  
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ACCESSION  
VERSION  
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ORGANISM

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Unpublished  
2 (bases 1 to 111945)  
EU Arabidopsis sequencing, project.  
Direct Submission  
Submitted (20-SEP-1999) MIPS, at the Max-Planck-Institut fuer  
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:  
schullee@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project  
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge  
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,  
E-mail: michael.bevan@bbsrc.ac.uk

JOURNAL  
AUTHORS  
TITLE  
JOURNAL

On Apr 18, 1998 this sequence version replaced gi:2982425.  
Information on performance of analysis and a more detailed  
annotation of this entry and other sequences of chromosomes 3, 4  
and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.  
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COMMENT

On Apr 18, 1998 this sequence version replaced gi:2982425.  
Information on performance of analysis and a more detailed  
annotation of this entry and other sequences of chromosomes 3, 4  
and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.

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Query Match  
Best Local Similarity 100.0%; Score 2030; DB 8; Length 111945;  
Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTAGAAGATCGACCATTTGAAGATACCTTCTCTTTCTATTATTTTATTATTATTAG 60  
Db 69711 CTTCTAGAAGATCGACCATTTGAAGATACCTTCTCTTTCTATTATTTTATTATTAG 69770

Qy 61 AAAATCATATTCATTACAAAAGAAAAAATAATTTTTGTATCTCTAAAGTTATAAC 120  
Db 69771 AAAATCATATTCATTACAAAAGAAAAAATAATTTTTGTATCTCTAAAGTTATAAC 69830

Qy 121 TTACAATTTTCACACTTCAGTTTGGTAGTATAATTAATCTATTTTATCAAAAGTTGG 180



69831 TTACAATTTTCCACACTTCAGTTGGTAGTATTAAATTTATCTATTTTATCAAAGTTTGG 69890  
181 TTTTAGGAAAAATGTATCTTTTCATATAAAAAATATATAGATCTTCAAAGAAATCTGAATT 240  
69891 TTTTAGGAAAAATGTATCTTTTCATATAAAAAATATATAGATCTTCAAAGAAATCTGAATT 69950  
241 GGGTTTTCAACTATTTTATCGTTTGGACACTACTTTTGACTTATCAAAAGAGTTCAAAATA 300  
69951 GGGTTTTCAACTATTTTATCGTTTGGACACTACTTTTGACTTATCAAAAGAGTTCAAAATA 70010  
301 GAAAAATAGAAATCGAAATCACACGTTTTCAGTGTAAAGAGGATTTTGATATTTGGTCGACATTT 360  
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361 TAAAGAGTTGTTTGTGTTTTTTTTTCCAAATCTGCAATGCGTTTTCGTTCCGTTGGAACCAAAAT 420  
70071 TAAAGAGTTGTTTGTGTTTTTTTTTCCAAATCTGCAATGCGTTTTCGTTCCGTTGGAACCAAAAT 70130  
421 TCAACACTTTGTATATAAACCAGTAATAGTATATACTAGAGTACGCGCAATACCAAAAATAAA 480  
70131 TCAACACTTTGTATATAAACCAGTAATAGTATATACTAGAGTACGCGCAATACCAAAAATAAA 70190  
481 ATTAATAACTCAATTCACAAATTTGAATCTACACCAATATCATGCATATATATCAGCAACCTA 540  
70191 ATTAATAACTCAATTCACAAATTTGAATCTACACCAATATCATGCATATATATCAGCAACCTA 70250  
541 GAATAATCAATGAAATTTAATFCAGGAGTAATCAATATATCCAACTCAACGATTAATCAAAGC 600  
70251 GAATAATCAATGAAATTTAATFCAGGAGTAATCAATATATCCAACTCAACGATTAATCAAAGC 70310  
601 CTAATAATAGATCAATGAAATCAAAATCACTAAACATAGTATATACATTTGTTGTTA 660  
70311 CTAATAATAGATCAATGAAATCAAAATCACTAAACATAGTATATACATTTGTTGTTA 70370  
661 AACAGAAATATATACATTTAATAGTATGAAATATGAATATATAGATTAAGAGGCGTA 720  
70371 AACAGAAATATATACATTTAATAGTATGAAATATGAATATATAGATTAAGAGGCGTA 70430  
721 TATGTTACAATCAGATCAGATCCCAATTAACAATCCGATTTGGTGGCGGCCATTTGTT 780  
70431 TATGTTACAATCAGATCAGATCCCAATTAACAATCCGATTTGGTGGCGGCCATTTGTT 70490  
781 TCGATATTTGCCCAACTGTTGATGATGACCTGCCAGCTGGCATATTTTCCCTCCTCGATT 840  
70491 TCGATATTTGCCCAACTGTTGATGATGACCTGCCAGCTGGCATATTTTCCCTCCTCGATT 70550  
841 ACGTTTTTACCCTTTCCCTCTCTGTTTCCACCGTTAAATTCAAATTTACTATTTGTACCGCT 900  
70551 ACGTTTTTACCCTTTCCCTCTCTGTTTCCACCGTTAAATTCAAATTTACTATTTGTACCGCT 70610  
901 GTCTTTACACCTTTTAAAGAAACCCAAACCGGAAATCAATACTATACGAAATCACATGT 960  
70611 GTCTTTACACCTTTTAAAGAAACCCAAACCGGAAATCAATACTATACGAAATCACATGT 70670  
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70671 CTTTCATCGTAGCTAACAAGACTTTATTTTCCGGTTGAAATTTGGTTTAACTTATGAGATT 70730  
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70731 GTGCTAACCGGAAACAGAAACCGTTTATGACGCCAACGAGGCAAGGGGTTAAACGAGAA 70790  
1081 AGGGGATGCGAGAAATCGTAATTAACAGGAAATTAAGGGTGGTTTTCAGATAAGTC 1140  
70791 AGGGGATGCGAGAAATCGTAATTAACAGGAAATTAAGGGTGGTTTTCAGATAAGTC 70850  
1141 TGTCTATATGACGCGAAAGGTTTCTTAAATTCAGAGAGCAATTAATCAGTTTCGTTG 1200  
70851 TGTCTATATGACGCGAAAGGTTTCTTAAATTCAGAGAGCAATTAATCAGTTTCGTTG 70910  
1201 TTTGGAGAAGAAGAACAGATCAAAATACGAGGAGATCTCTAAAGAGATTTATCGTT 1260  
70911 TTTGGAGAAGAAGAACAGATCAAAATACGAGGAGATCTCTAAAGAGATTTATCGTT 70970

1261 TCAAGTAAGTCTCTTTATCAAACTCTTAATATAAAAGAAATCAAAACATGACAGTCGTG 1320  
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1321 TCTTCGTTTCGATTTCTAGATACGATTTTTCGATGTTTCATGTCGAATCTCTGTTTTATTAC 1380  
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71091 TACTAGGGTTGTTCAATATTTTCCGAGAAATACCGAGAGAAACAAAGTTAGTGAATATAT 71150  
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71151 TGTATGAGATGAGTAAGTAATATATACATAAAATCATGTTTCTTCAAGCATCTACGT 71210  
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71211 TGAATATATATAAGAAAGTTTTCGTTGGTGAAGAAATATGATGAGAAAGTTTCATCTTTTC 71270  
1561 ATAATAGTGAACCAACTCTCTTCATACCAAAAAAAATTTGAAAAAAATTTAGTGAAA 1620  
71271 ATAATAGTGAACCAACTCTCTTCATACCAAAAAAAATTTGAAAAAAATTTAGTGAAA 71330  
1621 CTCTCTTTGTCGATTTAGGTTAGGTTGGACTCAGATCAAAATACGATTAGCATTAACAA 1680  
71331 CTCTCTTTGTCGATTTAGGTTAGGTTGGACTCAGATCAAAATACGATTAGCATTAACAA 71390  
1681 ATTTTTCGATGCGCAATTTATGTCGAGGTAAAAATATACCAATAGAAACATATTTTTC 1740  
71391 ATTTTTCGATGCGCAATTTATGTCGAGGTAAAAATATACCAATAGAAACATATTTTTC 71450  
1741 GAGTAGTTAAGATTATGATGAAGAAATCTATTTAGCATTAAGCATTAATAATTTTCTTTG 1800  
71451 GAGTAGTTAAGATTATGATGAAGAAATCTATTTAGCATTAAGCATTAATAATTTTCTTTG 71510  
1801 CTGTTCTGCTGTTTTCGTTTATGAACATTTGAATATGATCTTTTGTGTTTTTTTTCACC 1860  
71511 CTGTTCTGCTGTTTTCGTTTATGAACATTTGAATATGATCTTTTGTGTTTTTTTTCACC 71570  
1861 AGTAGATATGCTATATACACATAGTAACATGCGGTAGTTTATATAGAGAGAGATTGA 1920  
71571 AGTAGATATGCTATATACACATAGTAACATGCGGTAGTTTATATAGAGAGAGATTGA 71630  
1921 TTTTTCGTATATTTCTTTGTTGAAATAAATATGCTAAAAATTTATTTGTTTATTAATTT 1980  
71631 TTTTTCGTATATTTCTTTGTTGAAATAAATATGCTAAAAATTTATTTGTTTATTAATTT 71690  
1981 GACAGATTTCTTCACGTTGAGAAAGTTTAAATTTAGATTAAACCAACAAAAAG 2030  
71691 GACAGATTTCTTCACGTTGAGAAAGTTTAAATTTAGATTAAACCAACAAAAAG 71740

## RESULT 4

ATCHRIV52

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

REFERENCE

AUTHORS

198427 bp DNA linear PLN 16-MAR-2000  
Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52.

GI:7268789

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

1 (bases 1 to 82704)

Murphy, G., Ridley, P., Hudson, S., Mewes, H.W., Lemcke, K. and

Mayer, K.F.X.

Unpublished

2 (bases 67424 to 179368)

Terry, N., Ardles, W., Buysshaert, C., Daseville, R., De Clerck, R.,  
De Keyser, A., Neyt, P., Rouze, P., Van Den Daele, H., Villaroel, R.,

JOURNAL REFERENCE AUTHORS	Gielen, J., Van Montagu, M., Mewes, H.W., Lemcke, K. and Mayer, K.F.X. Unpublished 3 (bases 69292 to 69818) Voicckaert, G., Grymonprez, B., Voet, M., Robben, J., Mewes, H.W., Lemcke, K. and Mayer, K.F.X. Unpublished
JOURNAL REFERENCE AUTHORS	4 (bases 178975 to 187911) Mewes, H.W., Lemcke, K. and Mayer, K.F.X. Unpublished
JOURNAL REFERENCE AUTHORS	5 (bases 187649 to 198427) Pohl, T., Weizenegger, T., Mewes, H.W., Lemcke, K. and Mayer, K.F.X. Unpublished
JOURNAL REFERENCE AUTHORS	6 (bases 1 to 198427) EU Arabidopsis sequencing project. Direct Submission
TITLE JOURNAL	Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
COMMENT	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: <a href="http://www.mips.biochem.mpg.de/proj/thal/">http://www.mips.biochem.mpg.de/proj/thal/</a> this fragment has an overlap with ATCHRIV51 at the 5' end and an overlap with ATCHRIV53 at the 3' end.
FEATURES	Location/Qualifiers 1..198427 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /varity="Columbia" /db_xref="taxon:3702" /chromosome="4" 7547..8512 /gene="AT4g19950" join(7547..8329,8375..8512) /gene="AT4g19950" /note="similarity to p48 eggshell protein gene, Schistosoma mansoni, PATCHX:G454844 contains EST gb:AI994604.1, R30520, AI992766.1, T20423, AA712864, H76323" /codon_start=1 /product="putative protein" /protein_id="CAB78995.1" /db_xref="GI:7268790" /translation="MDLAPEELQFLNKGILRETSIPQYSLKTYLITLTLIFPLSF ATLAHSLTOPILADITVPOADQSOLOHEMTVLVFOFYIFLFAFSLSLSTAUVF TVASLYTGKVPFSSTMSNAIPLVXKLFTFLMWSLMLAYNTVFLIPLVTLI VAVDL QNVLAVSLVFLVFLVHVYMTALWHLASVNSVLEPIYGLAMKSYELLKGTLL NACSMVFYLVHCGFIAGVGVVGGDDYIGIFARI VAGGFLSVFYVYCKSFHHQEI DKSALHDHLGGYLGSEYPLKSNIQMENFEV" 7547..8329 /gene="AT4g19950" /number=1 8330..8374 /gene="AT4g19950" /number=1 8375..8512 /gene="AT4g19950" /number=2 11377..14567 /gene="AT4g19960" join(11377..11526,11621..11846,11925..12170,12258..12332, 12383..12643,12687..12887,12888,12986..13288,13407..13929, 14024..14567) /gene="AT4g19960" /note="similarity to putative potassium transporter AtKT2p & AtKtrp, Arabidopsis thaliana, Patchx:G2384669 & Patchx:G2384671 contains EST gb:AI997834.1" /codon_start=1 /product="potassium transporter-like protein"
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Qy	1561	ATAATAGTGAACAACCTCTCTTTTCATACCAAAAAAATTTTGAATAAATTTAGTGAA	1620
Ds	138694	ATAATAGTGAACAACCTCTCTTTTCATACCAAAAAAATTTTGAATAAATTTAGTGAA	138753
Qy	1621	CTCTCTTTGTCGCGATAGGTTAGGTTTGGACTCAGAAATCAAAAATACGATTAGCATACAA	1680
Ds	138754	CTCTCTTTGTCGCGATAGGTTAGGTTTGGACTCAGAAATCAAAAATACGATTAGCATACAA	138813
Qy	1681	ATTTTGGCGATGGCAATTTATGCTGCGAGTAAATATACCAATAGAAACATATTTTA	1740
Ds	138814	ATTTTGGCGATGGCAATTTATGCTGCGAGTAAATATACCAATAGAAACATATTTTA	138873
Qy	1741	GGAGTAGTAAAGATTATGATTGAAGAAATCTATTACGATAGCAATAAAATTTCTTTTG	1800
Ds	138874	GGAGTAGTAAAGATTATGATTGAAGAAATCTATTACGATAGCAATAAAATTTCTTTTG	138933
Qy	1801	CTGTTCTTTGGTTTTGTCGTTTTATAGAAATGTAATGATGACTTTTCTTTTTCACC	1860
Ds	138934	CTGTTCTTTGGTTTTGTCGTTTTATAGAAATGTAATGATGACTTTTCTTTTTCACC	138993
Qy	1861	AGTAGATAGTACTATACACATAGTAAGTAACATGGGTAGTTTATATAGAGAGAGATTGA	1920
Ds	138994	AGTAGATAGTACTATACACATAGTAAGTAACATGGGTAGTTTATATAGAGAGAGATTGA	139053
Qy	1921	TTTTTCGATATTTCTTTTGTGAAAAATAAATATGTAATAATTTATTTGTTTATTAATTT	1980
Ds	139054	TTTTTCGATATTTCTTTTGTGAAAAATAAATATGTAATAATTTATTTGTTTATTAATTT	139113
Qy	1981	GACAGATTGTTTCAGTTGAGAGTTTAAATTTAGATTAAACACAAAAAG	2030
Ds	139114	GACAGATTGTTTCAGTTGAGAGTTTAAATTTAGATTAAACACAAAAAG	139163
RESULT 5			
AX509457		1064 bp	DNA
LOCUS	AX509457	Sequence 4152 from Patent WO0216655.	linear PAT 27-SEP-2002
DEFINITION	AX509457		
ACCESSION	AX509457.1	GI:23390694	
VERSION			
KEYWORDS		Arabidopsis thaliana (thale cress)	
SOURCE		Arabidopsis thaliana	
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
REFERENCE		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
AUTHORS		rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
TITLE		Harper, J.F., Kreps, J., Wang, X. and Zhu, T.	
JOURNAL		Stress-regulated genes of plants, transgenic plants containing	
FEATURES		same, and methods of use	
source		Patent: WO 0216655-A 4152 28-FEB-2002;	
ORIGIN		The Scripps Research Institute (US); Syngenta Participations AG	
Query Match		(CH)	
Best Local Similarity		Location/Qualifiers	
Matches 1064; Conservative		1. .1064	
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		/mol_type="unassigned DNA"	
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		100.0%; Pred. No. 0;	
		0; Mismatches 0; Indels 0; Gaps 0;	
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Ds	1	GGTGACGTAAACAGACTTTATTTCCGGTTGAAATTTGGTTTAACTTATGAGATTGTGCTA	60
Qy	1027	ACCGAAACAGAAACGGTTATACGCCAACGAGGCGTAAGGGTAAACGACAAAGAGGG	1086
Ds	61	ACCGAAACAGAAACGGTTATACGCCAACGAGGCGTAAGGGTAAACGACAAAGAGGG	120
Qy	1087	GATGCGAGAAATCGTAAATTAACAGGAAATTAAGGGTGGTTTCAGATAAGCTGTGCTA	1146

Ds	121	GATGCGAGAAATCGTAAATTAACAGGAAATTAAGGGTGGTTTCCAGATAAGTCTGTCTA	180
Qy	1147	TATGACCGGAAAGGTTTCTTTAAATTCAGAGAGACAAATTAATCAGTTTCGTGTGTTTGG	1206
Ds	181	TATGACCGGAAAGGTTTCTTTAAATTCAGAGAGACAAATTAATCAGTTTCGTGTGTTTGG	240
Qy	1207	GAAGAAGAAACAGATCAAAATACGAGGAGAGATCTCTTAAAGAGATTATCGTTTCAAGT	1266
Ds	241	GAAGAAGAAACAGATCAAAATACGAGGAGAGATCTCTTAAAGAGATTATCGTTTCAAGT	300
Qy	1267	AAGTCTCTTTATCAAACTCTTAATATAAACAATCAAAACATGAACAGCTGCTGCTCG	1326
Ds	301	AAGTCTCTTTATCAAACTCTTAATATAAACAATCAAAACATGAACAGCTGCTGCTCG	360
Qy	1327	TTTCGATTCTAGATACGATTGTTTGTGTAATGAACTCTGTTTATTTACTACTAG	1386
Ds	361	TTTCGATTCTAGATACGATTGTTTGTGTAATGAACTCTGTTTATTTACTACTAG	420
Qy	1387	GGTTGTTCAATATTTTCCGAGAAATACAGAGGAAACAAAGTTAGTGATTATTTGATGC	1446
Ds	421	GGTTGTTCAATATTTTCCGAGAAATACAGAGGAAACAAAGTTAGTGATTATTTGATGC	480
Qy	1447	AGAGTATGAAGTAATATATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAT	1506
Ds	481	AGAGTATGAAGTAATATATACATAAATCATGTTTGTCTCAAGCATCTACGTTGAAT	540
Qy	1507	ATATATAAGAGATTGTTTGTGTAATGAACTCTGTTTATTTACTACTAG	1566
Ds	541	ATATATAAGAGATTGTTTGTGTAATGAACTCTGTTTATTTACTACTAG	600
Qy	1567	GTGAAACAACTCTCTTTCATACCAAAAAAATTTGAAAAAATTTAGTGAACCTCTCT	1626
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Qy	1627	TTGTCCGATTAGTTAGTTGGACTCAGAAATCAAAATACGATTAGCATACAAATTTT	1686
Ds	661	TTGTCCGATTAGTTAGTTGGACTCAGAAATCAAAATACGATTAGCATACAAATTTT	720
Qy	1687	TGGCATGGCAATTTATGTCGAGTAAATATACCAATAGAAACATATTTTACGAGTA	1746
Ds	721	TGGCATGGCAATTTATGTCGAGTAAATATACCAATAGAAACATATTTTACGAGTA	780
Qy	1747	GTTAAGATTATGATTGAAGAAATCTATTACGATAAGCATAAAAATTTCTTTGCTGTC	1806
Ds	781	GTTAAGATTATGATTGAAGAAATCTATTACGATAAGCATAAAAATTTCTTTGCTGTC	840
Qy	1807	TTGGTTTTGTCGTTTTATAGAACATTGCAATATGTAATTTGTTTTTCCACGATAGA	1866
Ds	841	TTGGTTTTGTCGTTTTATAGAACATTGCAATATGTAATTTGTTTTTCCACGATAGA	900
Qy	1867	TATGTACTATACACATAAGTAACATGGTAGTTTATATAGAGAGAGATTGATTTC	1926
Ds	901	TATGTACTATACACATAAGTAACATGGTAGTTTATATAGAGAGAGATTGATTTC	960
Qy	1927	GTATATTTCTTTTGTGTAATAAATATGTAATAATTTATTTGTTTATTAATTTGACAGA	1986
Ds	961	GTATATTTCTTTTGTGTAATAAATATGTAATAATTTATTTGTTTATTAATTTGACAGA	1020
Qy	1987	TTTGTTCAGTTGAGAGTTTAAATTTAGATTAAACACAAAAAG	2030
Ds	1021	TTTGTTCAGTTGAGAGTTTAAATTTAGATTAAACACAAAAAG	1064
RESULT 6			
AL807890/c		288 bp	DNA
LOCUS	AL807890	Arabidopsis thaliana transposon insertion STS SM_3.4802, sequence	linear STS 11-JUN-2003
DEFINITION	AL807890	tagged site.	
ACCESSION	AL807890		
VERSION	AL807890.1	GI:21690190	
KEYWORDS		STS; STS, sequence tagged site.	
SOURCE		Arabidopsis thaliana (thale cress)	
ORGANISM		Arabidopsis thaliana	

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1  
Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Murphy, G., Lingham, S., Legrys, C., Jones, J.D.G. and Bevan, M. Unpublished

2 (bases 1 to 288)

Clarke, J.H.

Direct Submission

Submitted (02-JUL-2002) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK

AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. \_3 denotes a sequence derived from the 3' end of the transposon, \_5 denotes a sequence derived from the 5' end of the transposon. B5SRC GARNET, ATIS project

On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock code: N109915.

FEATURES  
Location/Qualifiers  
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/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/variety="Columbia-0 NASC stock code N1092"  
/db\_xref="taxon:3702"  
/clone="AL022224"  
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STS  
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/standard\_name="SM\_3.4802"

ORIGIN  
Query Match 10.3%; Score 209; DB 11; Length 288;  
Best Local Similarity 100.0%; Pred. No. 2e-87;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 209 TAAATTCAGAGACAAATTAATCAGTTCGTGCTTTGGAGAGAGAGACAGATCAA 150

Qy 1227 ATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAAGTCTCTTTATCAAACTCT 1286  
Db 149 ATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAAGTCTCTTTATCAAACTCT 90

Qy 1287 TAAATTAACAACAAATCAAAACATGAACGTCGTGCTTCGTTTCGATTCTAGATACGATT 1346  
Db 89 TAAATTAACAACAAATCAAAACATGAACGTCGTGCTTCGTTTCGATTCTAGATACGATT 30

Qy 1347 TTTTAGTTCATGTGAATGAATCTGTTTT 1375  
Db 29 TTTTAGTTCATGTGAATGAATCTGTTTT 1

RESULT 7  
BX295033/c  
LOCUS  
DEFINITION  
Arabidopsis thaliana transposon insertion STS SM\_3.33484, sequence tagged site.  
ACCESSION  
BX295033  
VERSION  
BX295033.1 GI:29149723  
KEYWORDS  
STS; STS, sequence tagged site.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1  
Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Murphy, G., Lingham, S., Legrys, C., Jones, J.D.G. and Bevan, M. Unpublished

2 (bases 1 to 290)

Clarke, J.H.

Direct Submission

Submitted (20-MAR-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK

AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. \_3 denotes a sequence derived from the 3' end of the transposon, \_5 denotes a sequence derived from the 5' end of the transposon. B5SRC GARNET, ATIS project

On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock code: N120195.

FEATURES  
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/mol\_type="genomic DNA"  
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/db\_xref="taxon:3702"  
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/notes="Derived from superpool 1.28 NASC code N40027"

STS  
1..290  
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Best Local Similarity 100.0%; Pred. No. 2e-87;  
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Qy 1167 TAAATTCAGAGACAAATTAATCAGTTCGTGCTTTGGAGAGAGAGACAGATCAA 1226  
Db 209 TAAATTCAGAGACAAATTAATCAGTTCGTGCTTTGGAGAGAGAGACAGATCAA 150

Qy 1227 ATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAAGTCTCTTTATCAAACTCT 1286  
Db 149 ATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAAGTCTCTTTATCAAACTCT 90

Qy 1287 TAAATTAACAACAAATCAAAACATGAACGTCGTGCTTCGTTTCGATTCTAGATACGATT 1346  
Db 89 TAAATTAACAACAAATCAAAACATGAACGTCGTGCTTCGTTTCGATTCTAGATACGATT 30

Qy 1347 TTTTAGTTCATGTGAATGAATCTGTTTT 1375  
Db 29 TTTTAGTTCATGTGAATGAATCTGTTTT 1

RESULT 8  
AY086004  
LOCUS  
DEFINITION  
Arabidopsis thaliana clone 20592 mRNA, complete sequence.  
ACCESSION  
AY086004  
VERSION  
AY086004.1 GI:21404714  
KEYWORDS  
FLI CDNA.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1  
Haas, B.J., Volkovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve genome annotation

Genome Biol. 3 (6), RESEARCH0029 (2002)

2208475

12093376

2 (bases 1 to 1001)

Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.

Full-length cDNA from Arabidopsis thaliana

Unpublished

3 (bases 1 to 1001)

Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.

Direct Submission

Submitted (20-MAR-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK

AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. \_3 denotes a sequence derived from the 3' end of the transposon, \_5 denotes a sequence derived from the 5' end of the transposon. B5SRC GARNET, ATIS project

On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock code: N120195.

FEATURES  
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/clone="AL022224"  
/notes="Derived from superpool 1.28 NASC code N40027"

STS  
1..290  
/standard\_name="SM\_3.33484"

ORIGIN  
Query Match 10.3%; Score 209; DB 11; Length 290;  
Best Local Similarity 100.0%; Pred. No. 2e-87;  
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1167 TAAATTCAGAGACAAATTAATCAGTTCGTGCTTTGGAGAGAGAGACAGATCAA 1226  
Db 209 TAAATTCAGAGACAAATTAATCAGTTCGTGCTTTGGAGAGAGAGACAGATCAA 150

Qy 1227 ATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAAGTCTCTTTATCAAACTCT 1286  
Db 149 ATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAAGTAAAGTCTCTTTATCAAACTCT 90

Qy 1287 TAAATTAACAACAAATCAAAACATGAACGTCGTGCTTCGTTTCGATTCTAGATACGATT 1346  
Db 89 TAAATTAACAACAAATCAAAACATGAACGTCGTGCTTCGTTTCGATTCTAGATACGATT 30

Qy 1347 TTTTAGTTCATGTGAATGAATCTGTTTT 1375  
Db 29 TTTTAGTTCATGTGAATGAATCTGTTTT 1

RESULT 8  
AY086004  
LOCUS  
DEFINITION  
Arabidopsis thaliana clone 20592 mRNA, complete sequence.  
ACCESSION  
AY086004  
VERSION  
AY086004.1 GI:21404714  
KEYWORDS  
FLI CDNA.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1  
Haas, B.J., Volkovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve genome annotation

Genome Biol. 3 (6), RESEARCH0029 (2002)

2208475

12093376

2 (bases 1 to 1001)

Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.

Full-length cDNA from Arabidopsis thaliana

Unpublished

3 (bases 1 to 1001)

Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.

**TITLE**  
JOURNAL

**COMMENT**  
Direct Submission  
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA  
This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the WS or Llaer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genet carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

**FEATURES**  
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137..811  
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AEPPKP"

**CDS**  
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AEPPKP"

**ORIGIN**  
Query Match 4.5%; Score 91; DB 8; Length 1001;  
Best Local Similarity 100.0%; Pred. No. 1.3e-31;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1174 ACAGAGACAAATTAATCAGTTTCGTGTTGGAGAGAGAGAGACAGATCAATACGAG 1233  
DB 1 ACAGAGACAAATTAATCAGTTTCGTGTTGGAGAGAGAGAGACAGATCAATACGAG 60  
QY 1234 GAGAGATCTCTAAAGAGATTATCGTTTCAA 1264  
DB 61 GAGAGATCTCTAAAGAGATTATCGTTTCAA 91

**RESULT 9**  
AY093084  
LOCUS  
DEFINITION  
Arabidopsis thaliana endomembrane-associated protein (At4g20260)  
mRNA, complete cds.  
AY093084  
AY093084.1 GI:20260369  
FLI CDNA.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 1070)  
Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M.,  
Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H.,  
Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A.,  
Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K.,  
Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K.,  
Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.  
Direct Submission  
Submitted (27-MAR-2002) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,

**COMMENT**  
USA  
e-mail for correspondence: arab@sequence.stanford.edu  
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFI cDNAs (RAFI CDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.  
The Salk, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAFI cDNAs: Southwick, A., Nguyen, M., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.  
Southwick, A., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs.  
**FEATURES**  
Location/Qualifiers  
1..1070  
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/db\_xref="taxon:3702"  
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/clone="RAFI06-88-G20 (R17653)"  
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1..1070  
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/note="synonym: FIC12.180"  
127..804  
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VAEPPKP"

**ORIGIN**  
Query Match 3.9%; Score 79; DB 8; Length 1070;  
Best Local Similarity 100.0%; Pred. No. 6.3e-26;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1186 AATCAGTTTCGTGTTGGAGAGAGAGAGACAGATCAATACGAGAGATCTCTA 1245  
DB 3 AATCAGTTTCGTGTTGGAGAGAGAGAGACAGATCAATACGAGAGATCTCTA 62  
QY 1246 AAGAGATTATCGTTTCAA 1264  
DB 63 AAGAGATTATCGTTTCAA 81

**RESULT 10**  
ATENDASPR  
LOCUS  
DEFINITION  
A.thaliana mRNA for endomembrane-associated protein.  
Y08061  
Y08061.1 GI:1550737  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1  
Dupree, P., Prime, T.A. and Packman, L.C.  
Sequence of novel endomembrane-associated protein of Arabidopsis thaliana



JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1105)  
AUTHORS Dupree,P.  
TITLE Direct Submission  
JOURNAL Submitted (16-SEP-1996) P. Dupree, University of Cambridge,  
Department of Biochemistry, Tennis Court Road, Cambridge, CB2 1QW,  
UK

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VAEPPKP"

CDS

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Query Match 3.6%; Score 74; DB 8; Length 1105;  
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Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1191 GTTTCGTGTTGTCGAGAGAGAGACACATCAATACGAGAGATCTCTAAAGAG 1250  
Db 10 GTTTCGTGTTGTCGAGAGAGAGACACATCAATACGAGAGATCTCTAAAGAG 69  
Qy 1251 ATTATCGTTTCAA 1264  
Db 70 ATTATCGTTTCAA 83

RESULT 11  
AF083669 604 bp mRNA linear PLN 29-OCT-2002  
LOCUS Arabidopsis thaliana clone spe12 unknown mRNA.  
DEFINITION Arabidopsis thaliana  
ACCESSION AF083669  
VERSION AF083669.1 GI:24417235  
KEYWORDS  
SOURCE Arabidopsis thaliana (chale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
REFERENCE 1 (bases 1 to 604)  
AUTHORS Stracke,R. and Palme,K.  
TITLE Signal Peptide Selection derived cDNAs from Arabidopsis thaliana  
leaves and guard cells  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 604)  
AUTHORS Stracke,R. and Palme,K.  
TITLE Direct Submission  
JOURNAL Submitted (12-AUG-1998) Max-Delbrueck-Laboratorium in der  
Max-Planck-Gesellschaft, Carl-von-Linne-Weg 10, Koeln D-50829,  
Germany

FEATURES  
source Location/Qualifiers  
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CDS

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Query Match 2.9%; Score 58; DB 8; Length 604;  
Best Local Similarity 100.0%; Pred. No. 6e-16;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1207 GAAGAAGAAGAACAGATCAATACGAGAGATCTCTAAAGAGATTTATCGTTTCAA 1264  
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RESULT 12  
AF321237/c 111126 bp DNA linear PRI 20-JUN-2001  
LOCUS Homo sapiens chromosome 1p15.4 clone RPC11-610i20 P2-containing  
DEFINITION olfactory receptor gene cluster, complete sequence.  
ACCESSION AF321237  
VERSION AF321237.1 GI:12007433  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 111126)  
AUTHORS Lane,R.P., Cutforth,T., Young,J., Athanasiou,M., Friedman,C.,  
Rowen,L., Evans,G., Axel,R., Hood,L. and Trask,B.J.  
TITLE Genomic analysis of orthologous mouse and human olfactory receptor  
loci  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (13), 7390-7395 (2001)  
MEDLINE 21310002  
PUBMED 11416212  
REFERENCE 2 (bases 1 to 111126)  
AUTHORS Lane,R.P., Cutforth,T., Young,J., Athanasiou,M., Friedman,C.,  
Rowen,L., Evans,G., Axel,R., Hood,L. and Trask,B.J.  
TITLE Direct Submission  
JOURNAL Submitted (15-NOV-2000) Molecular Biotechnology, University of  
Washington, Seattle, WA 98195, USA  
COMMENT High-redundancy (7x) shotgun sequence of PAC 610i20 clone.  
Orthologous to the mouse chromosome-7E3 olfactory receptor cluster  
deposited in GenBank Accession Numbers AC321233 and AC321234.

FEATURES  
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CDS 4837..5763  
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FTFLRPGNSNIAHFFCEAPALLIIASTDTHASEMAIFLTGVVILLIPVFLIVSY  
GRIIVTVKMSVGSILKFEATCGSHLMVILEVGSALITYMTPKSSQKEKSVSVFY  
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CDS 104..>20743  
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complement (19796..>20743)





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* 33386 33485: gap of unknown length
* 33486 42561: contig of 9076 bp in length
* 42562 42661: gap of unknown length
* 42662 54313: contig of 11652 bp in length
* 54314 54413: gap of unknown length
* 54414 72085: contig of 17672 bp in length
* 72086 72185: gap of unknown length
* 72186 89296: contig of 17111 bp in length
* 89297 89396: gap of unknown length
* 89397 104805: contig of 15409 bp in length
* 104806 104905: gap of unknown length
* 104906 121851: contig of 16946 bp in length
* 121852 121951: gap of unknown length
* 121952 141389: contig of 19438 bp in length
* 141390 141489: gap of unknown length
* 141490 171660: contig of 30171 bp in length.
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        104906..121851
            /note="assembly_name:Contig17"
        121952..141389
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## ORIGIN

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Best Local Similarity 100.0%; Pident.No. 1.3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
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LOCUS          AC087280          173611 bp    DNA    linear    PRI 01-DEC-2001

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DEFINITION Homo sapiens chromosome 11, clone RP11-560B16, complete sequence.
ACCESSION AC087280
VERSION AC087280.11 GI:17223193
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173611)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-560B16
Unpublished
2 (bases 1 to 173611)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Baetien,V., Boguslavsky,L., Boukhgalter,B., Brown,A.,
Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
Collins,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Fero,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J.,
Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T.,
Lehoczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P.,
Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Norbu C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retra,R.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Teefaye,S., Theodore,J.,
Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-DEC-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 173611)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Baetien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chararo,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fero,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., McKernan,K., McPheeters,R., Meldrim,J.,
McCarthy,M., McEwan,P., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Meneus,L., Mihova,T., Mlenga,V., O'Connor,T., O'Donnell,P., O'Neil,D.,
Norbu,C., Norman,C.H., O'Neil,D., O'Neil,P., O'Neil,V.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retra,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Teefaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-DEC-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 1, 2001 this sequence version replaced gi:17047119.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information

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Center project name: L11843  
Center clone name: 560\_B\_16

FEATURES

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DB 31031 TTCATTACAAAGGAAAAAAAAAT 31055

RESULT 15

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SEQUENCE, 18 unordered pieces.  
AC027641  
AC027641.2 GI:8570385  
VERSION HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
208430 bp DNA linear HTG 07-JUL-2000

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 208430)  
Waterston,R.H.  
The sequence of Homo sapiens clone  
Unpublished  
2 (bases 1 to 208430)  
Waterston,R.H.  
Direct Submission  
Submitted (30-MAR-2000) Genome Sequencing Center, Washington  
University School of Medicine, 444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
On Jun 17, 2000 this sequence version replaced gi:7344780.

## COMMENT

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc/index.shtml>  
----- Project Information -----  
Center project name: H\_NH0732A19  
----- Summary Statistics -----  
Sequencing vector: M13; 984  
Chemistry: Dye-primer ET; 984 of reads  
Chemistry: Dye-terminator Big Dye; 24 of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 198825 bases at least Q40  
Consensus quality: 202103 bases at least Q30  
Consensus quality: 203934 bases at least Q20  
Insert size: 219000; agarose-fp  
Insert size: 206730; sum-of-contigs  
Quality coverage: 4.27 in Q20 bases; agarose-fp  
Quality coverage: 4.55 in Q20 bases; sum-of-contigs  
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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 18 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 1760: contig of 1760 bp in length  
\* 1761 1860: gap of unknown length  
\* 1861 3171: contig of 1311 bp in length  
\* 3172 3271: gap of unknown length  
\* 3272 5628: contig of 2357 bp in length  
\* 5629 5728: gap of unknown length  
\* 5729 7760: contig of 2032 bp in length  
\* 7761 7860: gap of unknown length  
\* 7861 15503: contig of 7643 bp in length  
\* 15504 15603: gap of unknown length  
\* 15604 18871: contig of 3268 bp in length  
\* 18872 18971: gap of unknown length  
\* 18972 2430: contig of 3459 bp in length  
\* 2431 28530: gap of unknown length  
\* 28531 28556: contig of 6026 bp in length  
\* 28557 28656: gap of unknown length  
\* 28657 35414: contig of 6758 bp in length  
\* 35415 35514: gap of unknown length  
\* 35515 42738: contig of 7224 bp in length  
\* 42739 42839: gap of unknown length  
\* 42839 50307: contig of 7469 bp in length  
\* 50308 50407: gap of unknown length  
\* 50408 62974: contig of 12567 bp in length  
\* 62975 63074: gap of unknown length  
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\* 73854 87730: contig of 13777 bp in length  
\* 87731 106802: contig of 19072 bp in length  
\* 106803 106902: gap of unknown length  
\* 106903 120650: contig of 13748 bp in length

\* 120651 120750: gap of unknown length  
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\* 156739 208430: contig of 51693 bp in length.

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## ORIGIN

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 70 TTCATTACAAAGGAAAAAAT 94  
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Db 100281 TTCATTACAAAGGAAAAAAT 100305

Search completed: October 24, 2005, 04:10:54  
Job time : 8849 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: October 23, 2005, 22:06:13 ; Search time 1095 Seconds  
(without alignment)  
10974.498 Million cell updates/sec

Title: US-10-643-676-1  
Perfect score: 2030  
Sequence: 1 cttcatgaagatggacca.....ttagattaaacacaaaaag 2030

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N Geneseq 16Dec04: \*  
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2: Geneseqn1990s: \*  
3: Geneseqn2000s: \*  
4: Geneseqn2001as: \*  
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6: Geneseqn2002as: \*  
7: Geneseqn2002bs: \*  
8: Geneseqn2003as: \*  
9: Geneseqn2003bs: \*  
10: Geneseqn2003cs: \*  
11: Geneseqn2003ds: \*  
12: Geneseqn2004as: \*  
13: Geneseqn2004bs: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	91	4.5	999	3	AAC49043	Arabidops
5	91	4.5	1001	3	AAC37034	Arabidops
6	89	4.4	495	3	AAC38110	Arabidops
7	83	4.1	515	3	AAC52118	Arabidops
8	53	2.6	1088	6	ABN98348	Arabidops
9	23	1.1	2550	11	ADM03675	Human cdn
10	22	1.1	427	6	ABL98998	Mouse neu
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12	22	1.1	432	4	AAI92210	Human pol
13	22	1.1	468	5	ABV60815	Human pro
14	22	1.1	2115	13	ADS51475	Bacterial
15	22	1.1	9607	2	AAV52213	Streptoco
16	22	1.1	110000	10	ABNS6454_01	Continuation (2 of
17	21	1.0	299	13	ADS51486	Bacterial
18	21	1.0	374	5	ADL41073	Human ova
19	21	1.0	429	4	AAI87584	Human pol
20	21	1.0	549	5	ADL43562	Human ova

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c 95	c 20	1.0	16918	6	ABL33617	Abi33617 Human imm	c 168	19	0.9	801	13	ADR05448	Adr05448 Hra3-C cd
c 96	c 20	1.0	22660	4	ABL09700	Abi09700 Drosophil	c 169	19	0.9	844	3	AAA26705	Aaa26705 Candida a
c 97	c 20	1.0	50657	13	ABD33455	Abd33455 Murine ca	c 170	19	0.9	845	2	AAT11323	Aat11323 DNA encod
c 98	c 20	1.0	60604	12	ADO48003	Ado48003 Human HIP	c 171	19	0.9	858	4	ABL10365	Abi10365 Drosophil
c 99	c 20	1.0	70708	12	ADQ97605	Adq97605 Human can	c 172	19	0.9	930	6	ABN93296	Abn93296 Staphyloc
c 100	c 20	1.0	77777	12	ADQ94674	Adq94674 Human chr	c 173	19	0.9	930	13	ADS04288	Adso4288 Staphyloc
c 101	c 20	1.0	84476	12	ADQ97028	Adq97028 Human can	c 174	19	0.9	955	6	AAI69492	Aai69492 A. sulcat
c 102	c 20	1.0	103929	3	AAF22287	Aaf22287 BAC conta	c 175	19	0.9	979	4	AAK61948	Aak61948 Human imm
c 103	c 20	1.0	110000	3	AAF22305_03	Continuation (4 of	c 176	19	0.9	1019	3	AAC96901	Aac96901 Human sec
c 104	c 20	1.0	110000	13	ABD32905_6	Continuation (7 of	c 177	19	0.9	1033	6	ABN98420	Abn98420 Arabidops
c 105	c 20	1.0	117754	11	ACN43866	Acn43866 Human gen	c 178	19	0.9	1038	6	ABN98420	Abn98420 Arabidops
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c 107	c 20	1.0	167771	6	ABQ88179	Abq88179 Human ost	c 180	19	0.9	1040	10	ADD55851	Add55851 Thalecres
c 108	c 20	1.0	204621	11	ACN44486	Acn44486 Human gen	c 181	19	0.9	1040	12	ADO01928	Ado01928 Thalecres
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c 113	c 19	0.9	103	6	ABK80027	Abk80027 Bacillus	c 186	19	0.9	1228	3	AAK79775	Aak79775 Human sec
c 114	c 19	0.9	140	3	AAK29478	Aak29478 Human sec	c 187	19	0.9	1327	12	ADK67712	Adk67712 Human mod
c 115	c 19	0.9	225	3	AAC41824	Aac41824 Arabidops	c 188	19	0.9	1337	12	ADJ27248	Adj27248 Human TRI
c 116	c 19	0.9	277	13	ACN52665	Acn52665 Corton an	c 189	19	0.9	1447	2	AAZ77457	Aaz77457 Human ova
c 117	c 19	0.9	289	4	AAI88427	Aai88427 Human pol	c 190	19	0.9	1451	6	ABK33940	Abk33940 Human DNA
c 118	c 19	0.9	343	10	ADD16308	Add16308 DNA (SeqI	c 191	19	0.9	1451	8	ADA20398	Ada20398 Prostate
c 119	c 19	0.9	352	6	ABL82126	Abi82126 Human ova	c 192	19	0.9	1451	8	ADAB4205	Ada84205 Human ren
c 120	c 19	0.9	352	8	ABX44964	Abx44964 Bovine ES	c 193	19	0.9	1478	3	AAZ51628	Aaz51628 Human mem
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c 123	c 19	0.9	369	4	AAI87529	Aai87529 Human pol	c 196	19	0.9	1666	8	ACC72435	Acc72435 Human sec
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c 125	c 19	0.9	381	5	ABV61901	Abv61901 Human pro	c 198	19	0.9	1789	2	AAI99226	Aai99226 Braesica
c 126	c 19	0.9	389	4	AAI87676	Aai87676 Human pol	c 199	19	0.9	1803	2	AAV31257	Aav31257 E. coli J
c 127	c 19	0.9	389	9	ACH29275	Ach29275 Human adu	c 200	19	0.9	1821	2	AAV22736	Aav22736 Babesia m
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c 135	c 19	0.9	413	5	ABV60954	Abv60954 Human pro	c 208	19	0.9	2000	8	ADA72550	Ada72550 Rice gene
c 136	c 19	0.9	418	4	AAI86360	Aai86360 Human pol	c 209	19	0.9	2033	3	AAK40796	Aac40796 Arabidops
c 137	c 19	0.9	419	9	ACH50072	Ach50072 Human leu	c 210	19	0.9	2135	6	ABK99840	Abk99840 Babesia c
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c 141	c 19	0.9	437	5	ABV31911	Abv31911 Human pro	c 214	19	0.9	2726	10	ADB62723	Adb62723 Human CDN
c 142	c 19	0.9	445	9	ACH17089	Ach17089 Human adu	c 215	19	0.9	2933	10	ADE56124	Ades6124 Rat gene
c 143	c 19	0.9	448	4	AAI86117	Aai86117 Human pol	c 216	19	0.9	2933	10	ADE56132	Ades6132 Rat gene
c 144	c 19	0.9	451	11	ADM65271	Adm65271 Human Y c	c 217	19	0.9	2933	10	ADE56136	Ades6136 Rat gene
c 145	c 19	0.9	461	2	AAV99639	Aav99639 Human t-p	c 218	19	0.9	2933	10	ADE56140	Ades6140 Rat gene
c 146	c 19	0.9	480	5	ABV10746	Abv10746 Human pro	c 219	19	0.9	2933	10	ADE56128	Ades6128 Rat gene
c 147	c 19	0.9	486	6	ABK74683	Abk74683 Bacillus	c 220	19	0.9	2970	13	ADR58928	Adr58928 Human Elk
c 148	c 19	0.9	501	6	ABN93117	Abn93117 Staphyloc	c 221	19	0.9	2981	10	ADE56120	Ades6120 Rat gene
c 149	c 19	0.9	501	13	ADS03995	Adso3995 Staphyloc	c 222	19	0.9	3047	4	AAH15890	Aah15890 Human CDN
c 150	c 19	0.9	507	5	ADL45017	Adl45017 Human ova	c 223	19	0.9	3047	4	AAH77801	Aah77801 Nucleotid
c 151	c 19	0.9	513	4	AAI86094	Aai86094 Human pol	c 224	19	0.9	3107	6	ABK33997	Abk33997 Human DNA
c 152	c 19	0.9	519	10	ADH84275	Adh84275 Enterococ	c 225	19	0.9	3107	8	ADA20429	Ada20429 Prostate
c 153	c 19	0.9	564	6	ABQ19371	Abq19371 Oligonuc	c 226	19	0.9	3107	8	ADA84236	Ada84236 Human ren
c 154	c 19	0.9	564	6	ABQ19370	Abq19370 Oligonuc	c 227	19	0.9	3374	4	ABL26932	Abi26932 Drosophil
c 155	c 19	0.9	566	5	ABV51724	Abv51724 Human pro	c 228	19	0.9	3410	4	AAH54074	Aah54074 S. epider
c 156	c 19	0.9	573	12	ADN74834	Adn74834 Thale cre	c 229	19	0.9	3474	4	AAH54494	Aah54494 S. epider
c 157	c 19	0.9	578	12	ACH73095	Ach73095 Human gen	c 230	19	0.9	3948	6	ABZ11243	Abz11243 Human pol
c 158	c 19	0.9	594	3	AAC54122	Aac54122 Arabidops	c 231	19	0.9	3948	12	ADM43761	Adm43761 Novel hum
c 159	c 19	0.9	596	6	ABN60109	Abn60109 Human can	c 232	19	0.9	4223	2	AAV22752	Aav22752 Babesia m
c 160	c 19	0.9	623	3	AAK35048	Aak35048 Arabidops	c 233	19	0.9	4223	2	AAV22737	Aav22737 Babesia m
c 161	c 19	0.9	631	6	ABQ52849	Abq52849 Oligonuc	c 234	19	0.9	4223	2	AAK90001	Aax90001 Babesia m
c 162	c 19	0.9	631	6	ABQ52848	Abq52848 Oligonuc	c 235	19	0.9	4223	2	AAK90015	Aax90015 Babesia m
c 163	c 19	0.9	664	4	AAK71302	Aak71302 Human imm	c 236	19	0.9	4223	3	AAK65098	Aac65098 B. microt
c 164	c 19	0.9	696	11	ACN91654	Acn91654 Breast ca	c 237	19	0.9	4223	3	AAK65084	Aac65084 B. microt
c 165	c 19	0.9	744	2	AAK20367	Aax20367 Borrelia	c 238	19	0.9	4223	6	ABL89342	Abi89342 Babesia m
c 166	c 19	0.9	767	6	ABQ21778	Abq21778 Oligonuc	c 239	19	0.9	4223	6	ABL89328	Babesia m

240	19	0.9	4223	8	ACA92623	313	19	0.9	17421	4	AAS45349	Aas45349	Chemical
C 241	19	0.9	4223	8	ACA92637	C 314	19	0.9	17421	4	AAS45349	Aas45349	Chemical
C 242	19	0.9	4223	10	ADE05991	C 315	19	0.9	17421	6	ABK28182	Abk28182	DNA trans
C 243	19	0.9	4223	10	ADE06190	C 316	19	0.9	17421	6	ABK28182	Abk28182	DNA trans
C 244	19	0.9	4945	4	ABL02632	C 317	19	0.9	17491	6	ABL34574	AbL34574	Human met
C 245	19	0.9	5129	12	ADM67113	C 318	19	0.9	17491	7	ADN99835	Adn99835	Bisulphite
C 246	19	0.9	5129	13	ADR99019	C 319	19	0.9	17534	6	ABK40026	Abk40026	Human che
C 247	19	0.9	5338	6	ABK11379	C 320	19	0.9	17721	6	ABL33728	AbL33728	Human che
C 248	19	0.9	5338	6	ABK11379	C 321	19	0.9	17970	6	ABQ67034	AbQ67034	Human ang
C 249	19	0.9	5338	6	ABL70330	C 322	19	0.9	18133	6	ABK40017	AbK40017	Human che
C 250	19	0.9	5442	6	AAS61281	C 323	19	0.9	18133	6	ABL32940	AbL32940	Human imm
C 251	19	0.9	5569	4	ABL33968	C 324	19	0.9	18357	6	ABQ67084	AbQ67084	Human ang
C 252	19	0.9	5807	6	ABL10364	C 325	19	0.9	19441	4	AAK80351	Aak80351	Human imm
C 253	19	0.9	6047	6	ABL33154	C 326	19	0.9	21500	11	ACN43960	Acn43960	Mouse gen
C 254	19	0.9	6118	6	ABL33459	C 327	19	0.9	25179	13	ABD33248	Abd33248	Murine ca
C 255	19	0.9	6126	6	ABL33445	C 328	19	0.9	28118	10	ADE43798	Ade43798	Polymorph
C 256	19	0.9	6126	6	ABL33135	C 329	19	0.9	28118	10	ADE43797	Ade43797	Human TNF
C 257	19	0.9	6215	6	ABL33190	C 330	19	0.9	28118	12	ADH54276	Adh54276	Human TNF
C 258	19	0.9	6240	6	ABL32137	C 331	19	0.9	28118	12	ADH54275	Adh54275	Human TNF
C 259	19	0.9	6240	6	ABL34455	C 332	19	0.9	29993	10	ADB37663	Adb37663	Human che
C 260	19	0.9	6240	7	ADS99716	C 333	19	0.9	29993	10	ADB37661	Adb37661	Human che
C 261	19	0.9	6270	6	ABL33873	C 334	19	0.9	38342	4	AAS46746	Aas46746	Tumour eu
C 262	19	0.9	6837	6	AAD29902	C 335	19	0.9	38342	6	ABK31507	Abk31507	Signal tr
C 263	19	0.9	6866	6	ABL32667	C 336	19	0.9	45121	9	ADA02744	Ada02744	Human TNF
C 264	19	0.9	6866	6	ABL49320	C 337	19	0.9	45121	10	ADB72482	Adb72482	Human TNF
C 265	19	0.9	6988	6	ABL34441	C 338	19	0.9	45121	10	ADC85224	Adc85224	Human Trf
C 266	19	0.9	7058	6	ABK40051	C 339	19	0.9	45121	12	ADM74339	Adm74339	Human car
C 267	19	0.9	7083	4	ABL02670	C 340	19	0.9	52616	4	AAK70459	Aak70459	Human imm
C 268	19	0.9	7322	11	ACN92378	C 341	19	0.9	52616	4	AAK78930	Aak78930	Human imm
C 269	19	0.9	7522	6	ABL32915	C 342	19	0.9	55829	13	ABD33512	Abd33512	Human can
C 270	19	0.9	7544	4	AAS45301	C 343	19	0.9	60500	11	ACN44530	Acn44530	Human gen
C 271	19	0.9	7832	6	ABK67847	C 344	19	0.9	65464	8	ABX13172	Abx13172	Continuation (4 of
C 272	19	0.9	8103	6	ABL33661	C 345	19	0.9	68004	6	ABL57909	AbL57909	3
C 273	19	0.9	8168	6	ABL32929	C 346	19	0.9	71678	11	ACN44284	Acn44284	Mouse gen
C 274	19	0.9	8168	6	ABL32929	C 347	19	0.9	73334	6	ABL34124	AbL34124	Human imm
C 275	19	0.9	8168	6	AAS63328	C 348	19	0.9	73334	6	ABL92318	AbL92318	Chemical
C 276	19	0.9	8168	6	AAS63329	C 349	19	0.9	73742	12	ADQ97824	Adq97824	Human can
C 277	19	0.9	8514	4	AAK61530	C 350	19	0.9	76416	10	ADL13662	AdL13662	Osteoarthritis
C 278	19	0.9	8530	6	ABL32432	C 351	19	0.9	76600	12	ADO79402	Ado79402	regl
C 280	19	0.9	8758	6	ABL33118	C 352	19	0.9	82938	6	ABV72623	Abv72623	Human tra
C 281	19	0.9	8876	6	ABL34076	C 353	19	0.9	83180	11	ACN44784	Acn44784	Mouse gen
C 282	19	0.9	8915	4	ABL29664	C 354	19	0.9	90220	11	ABK83576	Abk83576	Human cdn
C 283	19	0.9	9390	4	ABL13248	C 355	19	0.9	93483	9	ADA03083	Ada03083	Mouse mCG
C 284	19	0.9	9728	6	ABK40092	C 356	19	0.9	93483	9	ADA66367	Ada66367	Mouse mCG
C 285	19	0.9	9728	6	ABK33903	C 357	19	0.9	93483	10	ADB72821	Adb72821	Mouse gen
C 286	19	0.9	9914	9	ADB60827	C 358	19	0.9	93483	11	ADL27161	AdL27161	Human gen
C 287	19	0.9	9914	9	ABL32695	C 359	19	0.9	95835	11	ACN45042	Acn45042	Human gen
C 288	19	0.9	9963	6	ABN80083	C 360	19	0.9	96594	10	ADE95974	AdE95974	Human SYK
C 289	19	0.9	10250	6	ABL32335	C 361	19	0.9	96595	9	ADA02726	Ada02726	Human SYK
C 290	19	0.9	10528	6	AAS44199	C 362	19	0.9	96960	10	ADB72464	AdB72464	Human SYK
C 291	19	0.9	10815	2	AAV441199	C 363	19	0.9	96960	8	ACF62734	AcF62734	Cancer ba
C 292	19	0.9	10815	6	ABK67796	C 364	19	0.9	96960	8	ADB20849	AdB20849	MRP1 base
C 293	19	0.9	11049	6	ABL92221	C 365	19	0.9	96960	10	ADB87938	AdB87938	Human UGT
C 294	19	0.9	11049	6	ABL49324	C 366	19	0.9	96960	10	ADB96921	AdB96921	Human MDR
C 295	19	0.9	11670	6	ABL54325	C 367	19	0.9	96960	10	ADB92112	AdB92112	Human MDR
C 296	19	0.9	12816	4	ABL20852	C 368	19	0.9	98844	7	ADJ84039	AdJ84039	Human WRN
C 297	19	0.9	12986	4	AAS46554	C 369	19	0.9	100000	6	ABQ74541	AbQ74541	Human tra
C 298	19	0.9	13149	2	AAV44231	C 370	19	0.9	107280	13	ABD33169	Abd33169	Murine ca
C 299	19	0.9	13149	6	ABK67843	C 371	19	0.9	107280	13	ABD32933	Abd32933	Mouse can
C 300	19	0.9	13339	2	AAV44234	C 372	19	0.9	108566	13	AAS58840	Aas58840	Mycoplasma
C 301	19	0.9	13449	6	ABL33385	C 373	19	0.9	110000	2	ABX08336	AbX08336	14
C 302	19	0.9	14491	8	ABZ10061	C 374	19	0.9	110000	6	ABX08336	AbX08336	14
C 303	19	0.9	14491	8	ABZ10207	C 375	19	0.9	110000	10	ABG70447	AbG70447	3
C 304	19	0.9	14491	13	ADS89667	C 376	19	0.9	110000	10	ABG79565	AbG79565	3
C 305	19	0.9	14913	13	ADS89667	C 377	19	0.9	110000	11	ACN43988	Acn43988	3
C 306	19	0.9	15122	6	ABL32775	C 378	19	0.9	110000	11	ACN43988	Acn43988	4
C 307	19	0.9	15861	6	ABL32524	C 379	19	0.9	110000	12	ADJ25985	AdJ25985	14
C 308	19	0.9	16127	6	ABL32745	C 380	19	0.9	110000	12	ADN97989	AdN97989	14
C 309	19	0.9	16173	6	ABL34468	C 381	19	0.9	110000	12	ADO50281	AdO50281	14
C 310	19	0.9	16173	7	ADS99729	C 382	19	0.9	11950	2	AAK90201	Aak90201	Human yes
C 311	19	0.9	16688	4	AAS46555	C 383	19	0.9	122923	11	ACN44026	Acn44026	Human gen
C 312	19	0.9	17141	6	AAD26486	C 384	19	0.9	143412	11	ACN44512	Acn44512	Mouse gen
	19	0.9				C 385	19	0.9	145985	12	ADQ97164	AdQ97164	Human can
	19	0.9					19	0.9	146733	12	ADQ97410	AdQ97410	Mouse can



c 386 19 0.9 150830 12 ADQ97260 Adq97260 Mouse can  
c 387 19 0.9 152501 12 ADP67269 Adp67269 Human chr  
388 19 0.9 154465 6 AAD28763 Aad28763 Human AKA  
389 19 0.9 158245 6 AAD28762 Aad28762 Human AKA  
390 19 0.9 161425 4 AAH02340 Aah02340 Human AKA  
391 19 0.9 162025 4 AAH02339 Aah02339 Human AKA  
392 19 0.9 162025 6 AAD28758 Aad28758 Human AKA  
393 19 0.9 162025 6 AAD28759 Aad28759 Human AKA  
394 19 0.9 162025 13 ADS75958 Adg75958 Human A-k  
395 19 0.9 162025 13 ADS75959 Adg75959 Human A-k  
396 19 0.9 162025 13 ADS75963 Adg75963 Human A-k  
397 19 0.9 162025 13 ADS75962 Adg75962 Human A-k  
c 398 19 0.9 171324 11 ACN43892 Acn43892 Mouse gen  
c 399 19 0.9 177866 10 ADL13935 Adl13935 Osteoarth  
c 400 19 0.9 180227 13 ABD33268 Abd33268 Human can  
c 401 19 0.9 180550 10 ADL13850 Adl13850 Osteoarth  
c 402 19 0.9 198285 6 ABK84699 Abk84699 Human cdn  
c 403 19 0.9 198285 6 ABN97319 Abn97319 Gene #381  
c 404 19 0.9 198285 13 ADR52987 Adr52987 Drug ther  
c 405 19 0.9 224112 13 ABD32600 Abd32600 Mouse can  
c 406 19 0.9 235033 2 AAV57926 Aav57926 Hereditar  
c 407 19 0.9 237326 2 AAV57903 Aav57903 Hereditar  
c 408 19 0.9 277616 13 ABD32602 Abd32602 Human can  
c 409 19 0.9 290547 13 ABD32598 Abd32598 Human can  
c 410 19 0.9 304326 13 ADS15253 Ads15253 Rat senso  
c 411 19 0.9 304905 11 ADP75180 Adp75180 Human end  
c 412 19 0.9 330973 11 ACN44846 Acn44846 Human gen  
c 413 18 0.9 50 4 AA174541 Aai74541 Human sll  
c 414 18 0.9 51 4 AAL29390 Aal29390 Human SNP  
c 415 18 0.9 51 4 AAL29391 Aal29391 Human SNP  
c 416 18 0.9 64 2 AAT23945 Aat23945 Human gen  
c 417 18 0.9 153 13 ACN61614 Acn61614 Cotton gy  
c 418 18 0.9 169 3 AAA44502 Aaa44502 Human sec  
c 419 18 0.9 171 6 ABN70060 Abn70060 Streptoco  
c 420 18 0.9 174 4 AAL04406 Aal04406 Human tep  
c 421 18 0.9 174 10 ABX61003 Abx61003 Arabidops  
c 422 18 0.9 195 6 ADH31656 Adh31656 Novel yea  
c 423 18 0.9 206 6 ABN20116 Abn20116 Human ORF  
c 424 18 0.9 217 3 AAC22600 Aac22600 Human sec  
c 425 18 0.9 218 12 ACH90719 Ach90719 Human gen  
c 426 18 0.9 231 6 ABN72980 Abn72980 Clone 077  
c 427 18 0.9 231 9 ADA08621 Ada08621 Human O77  
c 428 18 0.9 231 10 ADF08964 Adf08964 CDNA enco  
c 429 18 0.9 238 10 ABX83935 Abx83935 Corn ear-  
c 430 18 0.9 246 6 ABN91640 Abn91640 Staphyloc  
c 431 18 0.9 246 13 ADS02669 Ads02669 Staphyloc  
c 432 18 0.9 258 4 AAK57482 Aak57482 Human imm  
c 433 18 0.9 269 3 AAA41830 Aaa41830 Human sec  
c 434 18 0.9 287 12 ADP92817 Adp92817 Cotton ex  
c 435 18 0.9 302 9 ACC72342 Acc72342 Human cdn  
c 436 18 0.9 315 4 AA191643 Aai91643 Human pol  
c 437 18 0.9 316 6 ABN75585 Abn75585 Human ORF  
c 438 18 0.9 330 5 ADI71884 Adi71884 Human ova  
c 439 18 0.9 330 5 ADL37035 Adl37035 Human ova  
c 440 18 0.9 333 5 ABV61653 Abv61653 Human pro  
c 441 18 0.9 336 6 ABN91228 Abn91228 Staphyloc  
c 442 18 0.9 336 13 ADS01437 Ads01437 Staphyloc  
c 443 18 0.9 339 5 ABV12927 Abv12927 Human pro  
c 444 18 0.9 339 6 ABN90677 Abn90677 Staphyloc  
c 445 18 0.9 343 13 ADS03881 Ads03881 Staphyloc  
c 446 18 0.9 343 4 AAI88988 Aai88988 Human pol  
c 447 18 0.9 353 4 AAS38160 Aas38160 Novel hum  
c 448 18 0.9 357 4 AAK90758 Aak90758 Human dig  
c 449 18 0.9 357 4 AAK90757 Aak90757 Human dig  
c 450 18 0.9 357 4 AAK90760 Aak90760 Human dig  
c 451 18 0.9 359 2 AAV70867 Aav70867 Internal  
c 452 18 0.9 366 5 ABV03758 Abv03758 Human pro  
c 453 18 0.9 366 9 ACH42695 Ach42695 Human foe  
c 454 18 0.9 367 5 ABV11422 Abv11422 Human pro  
c 455 18 0.9 368 6 ABN73683 Abn73683 Bovine em  
c 456 18 0.9 369 3 AAC20944 Aac20944 Human sec  
c 457 18 0.9 369 6 ABK76527 Abk76527 Bacillus  
c 458 18 0.9 373 10 ADI81900 Adi81900 A. thalia

c 459 18 0.9 380 4 AAI88638 Aai88638 Human pol  
c 460 18 0.9 384 6 ABQ85232 Abq85232 Arabidops  
c 461 18 0.9 385 5 ADI74507 Adi74507 Human ova  
c 462 18 0.9 385 5 ADI68136 Adi68136 Human ova  
c 463 18 0.9 390 4 AAE24796 Aae24796 Human ova  
c 464 18 0.9 390 4 AAS25234 Aas25234 Human ova  
c 465 18 0.9 391 5 ABV37425 Abv37425 Human pro  
c 466 18 0.9 393 5 ADI74443 Adi74443 Human ova  
c 467 18 0.9 393 5 ADI68071 Adi68071 Human ova  
c 468 18 0.9 394 5 ADI74256 Adi74256 Human ova  
c 469 18 0.9 394 5 ADI67879 Adi67879 Human ova  
c 470 18 0.9 396 5 ABV00134 Abv00134 Human pro  
c 471 18 0.9 397 4 AAS24967 Aas24967 Human ova  
c 472 18 0.9 398 4 AAS25164 Aas25164 Human ova  
c 473 18 0.9 400 5 ABV47292 Abv47292 Human pro  
c 474 18 0.9 401 4 AAI87600 Aai87600 Human pol  
c 475 18 0.9 402 6 ABN94866 Abn94866 Gene #136  
c 476 18 0.9 404 4 AAI92214 Aai92214 Human pol  
c 477 18 0.9 404 9 ACH21593 Ach21593 Human adu  
c 478 18 0.9 407 8 ABX62545 Abx62545 Arabidops  
c 479 18 0.9 408 9 ACH16506 Ach16506 Human adu  
c 480 18 0.9 408 13 ACN56309 Acn56309 Cotton an  
c 481 18 0.9 409 5 ADL43419 Adl43419 Human ova  
c 482 18 0.9 409 9 ACH16770 Ach16770 Human adu  
c 483 18 0.9 410 5 ABV56396 Abv56396 Human pro  
c 484 18 0.9 412 4 AAK60606 Aak60606 Human imm  
c 485 18 0.9 412 5 AAI93150 Aai93150 Human pol  
c 486 18 0.9 415 5 ADI70165 Adi70165 Human ova  
c 487 18 0.9 415 5 ADI76494 Aai76494 Human ova  
c 488 18 0.9 416 4 AAI86045 Aai86045 Human pol  
c 489 18 0.9 416 6 ABV94293 Abv94293 Breast ca  
c 490 18 0.9 418 5 ABV02253 Abv02253 Human pro  
c 491 18 0.9 423 10 ADS56582 Ads56582 Toxicity-  
c 492 18 0.9 423 12 ADP72059 Adp72059 Renal tox  
c 493 18 0.9 426 5 ADL44606 Adl44606 Human ova  
c 494 18 0.9 428 5 ABV14216 Abv14216 Human pro  
c 495 18 0.9 430 4 AAI85300 Aai85300 Human pol  
c 496 18 0.9 430 9 ACH19136 Ach19136 Human adu  
c 497 18 0.9 432 8 ABX61999 Abx61999 Arabidops  
c 498 18 0.9 434 6 ABS69631 Abs69631 Novel mur  
c 499 18 0.9 434 8 ABX38360 Abx38360 Bovine ES  
c 500 18 0.9 435 5 ADL39641 Adl39641 Human ova  
c 501 18 0.9 441 5 ADL39738 Adl39738 Human ova  
c 502 18 0.9 442 4 AAI92484 Aai92484 Human pol  
c 503 18 0.9 444 1 AAN91069 Aan91069 Cloned cd  
c 504 18 0.9 444 5 ADI75137 Adi75137 Human ova  
c 505 18 0.9 445 8 ABX54049 Abx54049 Bovine ES  
c 506 18 0.9 445 8 ABX54049 Abx54049 Bovine ES  
c 507 18 0.9 446 5 ADI68761 Adi68761 Human ova  
c 508 18 0.9 446 5 ADI75120 Adi75120 Human ova  
c 509 18 0.9 446 10 ADH69123 Adh69123 Human tum  
c 510 18 0.9 447 5 ABV05047 Abv05047 Human pro  
c 511 18 0.9 448 4 AAS24989 Aas24989 Human ova  
c 512 18 0.9 448 13 ACN56120 Acn56120 Cotton an  
c 513 18 0.9 456 5 ABV09280 Abv09280 Human pro  
c 514 18 0.9 462 5 ADI68152 Adi68152 Human ova  
c 515 18 0.9 462 5 ADI74523 Adi74523 Human ova  
c 516 18 0.9 462 9 ACH26701 Ach26701 Human adu  
c 517 18 0.9 463 5 ABV30456 Abv30456 Human pro  
c 518 18 0.9 463 5 ABV68779 Abv68779 Human ova  
c 519 18 0.9 463 5 ADI75138 Adi75138 Human ova  
c 520 18 0.9 463 10 ADH69126 Adh69126 Human tum  
c 521 18 0.9 464 4 AAI15472 Aai15472 Probe #54  
c 522 18 0.9 464 4 ABA57311 Aab57311 Human foe  
c 523 18 0.9 464 4 AAI36853 Aai36853 Probe #55  
c 524 18 0.9 464 4 ABA26863 Aab26863 Probe #53  
c 525 18 0.9 464 4 AAK30940 Aak30940 Human bon  
c 526 18 0.9 464 4 AAK05346 Aak05346 Human bra  
c 527 18 0.9 464 4 AAS30618 Aas30618 Human liv  
c 528 18 0.9 464 6 ABS05688 Abs05688 Human gen  
c 529 18 0.9 465 4 AAS24842 Aas24842 Human ova  
c 530 18 0.9 465 4 AAS25281 Aas25281 Human ova  
c 531 18 0.9 466 5 ADI68707 Adi68707 Human ova

532	18	0.9	466	5	ADI75068	Adi75068 Human ova	605	18	0.9	557	5	ABV41361	Abv41361 Human pro
533	18	0.9	467	5	ADI75039	Adi75039 Human ova	606	18	0.9	557	5	ABV44061	Abv44061 Human pro
534	18	0.9	467	5	ADI68677	Adi68677 Human ova	607	18	0.9	557	5	ADL42218	Adl42218 Human ova
C 535	18	0.9	468	5	ABV56200	Abv56200 Human pro	608	18	0.9	558	5	ADL40284	Adl40284 Human ova
C 536	18	0.9	469	5	ADL39744	Adl39744 Human ova	C 609	18	0.9	561	4	AA525018	Aa525018 Human ova
C 537	18	0.9	470	3	AAC37252	Aac37252 Arabidops	C 610	18	0.9	561	12	ADO63628	Ado63628 Tranecrip
538	18	0.9	470	5	ABV42919	Abv42919 Human pro	C 611	18	0.9	571	5	AAH83634	Aah83634 Human ova
539	18	0.9	470	5	ABV34052	Abv34052 Human pro	C 612	18	0.9	571	5	ABV35222	Abv35222 Human pro
540	18	0.9	470	5	ABV41492	Abv41492 Human pro	C 613	18	0.9	573	4	AAH29095	Aah29095 Drosophil
541	18	0.9	470	5	ABV32567	Abv32567 Human pro	C 614	18	0.9	573	5	ADL40303	Adl40303 Human ova
542	18	0.9	470	5	ADI67875	Adi67875 Human ova	615	18	0.9	573	8	ACA39244	Aca39244 Prokaryot
543	18	0.9	470	5	ADL74252	Adl74252 Human ova	616	18	0.9	574	4	ABA88607	Aba88607 Escherich
544	18	0.9	477	5	ADI40365	Adi40365 Human ova	617	18	0.9	575	8	ABZ75570	Abz75570 Rice albu
545	18	0.9	478	9	ACH48211	Ach48211 Human lun	618	18	0.9	583	5	ADL40276	Adl40276 Human ova
C 546	18	0.9	479	5	ABV35310	Abv35310 Human pro	619	18	0.9	587	6	ABO20070	Abg20070 Oligonuc
C 547	18	0.9	479	5	ABV44142	Abv44142 Human pro	C 620	18	0.9	587	6	ABQ20071	Abq20071 Oligonuc
C 548	18	0.9	480	4	AAS24748	Aas24748 Human ova	C 621	18	0.9	588	6	ABQ52101	Abq52101 Oligonuc
C 549	18	0.9	480	5	AAH83378	Aah83378 Human ova	C 622	18	0.9	588	6	ABQ52100	Abq52100 Oligonuc
C 550	18	0.9	480	5	ADL38878	Adl38878 Human ova	C 623	18	0.9	594	4	AAK88246	Aak88246 Human dig
C 551	18	0.9	481	5	ADI72202	Adi72202 Human ova	C 624	18	0.9	594	5	AAK88246	Aak88246 Human dig
C 552	18	0.9	482	5	ABV49155	Abv49155 Human pro	C 625	18	0.9	594	5	AAK88246	Aak88246 Human dig
C 553	18	0.9	483	12	ADQ18576	Adq18576 Human sof	C 626	18	0.9	594	12	ACH77007	Ach77007 Human nov
C 554	18	0.9	485	5	AAH83479	Aah83479 Human ova	C 627	18	0.9	595	5	AAH55848	Aah55848 Human SCN
555	18	0.9	485	6	AA561517	Aas61517 Lung smal	C 628	18	0.9	598	10	ADK54516	Adk54516 Plant DNA
556	18	0.9	486	5	ADL39760	Adl39760 Human ova	C 629	18	0.9	600	5	ABV14127	Abv14127 Human pro
557	18	0.9	488	5	ADI68705	Adi68705 Human ova	630	18	0.9	601	5	ABV11286	Abv11286 Human pro
558	18	0.9	488	5	ADI75066	Adi75066 Human ova	C 631	18	0.9	602	6	ABO50531	Abq50531 Oligonuc
C 559	18	0.9	488	5	ADI75148	Adi75148 Human ova	C 632	18	0.9	602	6	ABQ50530	Abq50530 Oligonuc
C 560	18	0.9	488	5	ADI68789	Adi68789 Human ova	C 633	18	0.9	606	3	AAA16055	Aaa16055 Human col
C 561	18	0.9	488	10	ADH69125	Adh69125 Human tum	C 634	18	0.9	609	4	AAV09303	Abv09303 Human col
C 562	18	0.9	490	4	AAI91741	Aai91741 Human pol	C 635	18	0.9	609	4	AAV09303	Abv09303 Human col
563	18	0.9	491	12	ADQ20053	Adq20053 Human sof	C 636	18	0.9	609	4	AAV09303	Abv09303 Human col
564	18	0.9	492	5	ADL40336	Adl40336 Human ova	C 637	18	0.9	609	5	AAH83481	Aah83481 Human ova
C 565	18	0.9	494	5	AAH83612	Aah83612 Human ova	C 638	18	0.9	609	5	AAH83481	Aah83481 Human ova
C 566	18	0.9	497	5	ADI68714	Adi68714 Human ova	C 639	18	0.9	614	5	ADL36674	Adl36674 Human ova
567	18	0.9	497	5	ADI75075	Adi75075 Human ova	640	18	0.9	614	5	ADL36674	Adl36674 Human ova
568	18	0.9	497	10	ADH69124	Adh69124 Human tum	C 641	18	0.9	622	4	AAV20340	Aav20340 Human bre
569	18	0.9	498	5	ADI68770	Adi68770 Human ova	C 642	18	0.9	622	4	AAV20340	Aav20340 Human bre
570	18	0.9	498	5	ADI75129	Adi75129 Human ova	C 643	18	0.9	622	4	AAV20340	Aav20340 Human bre
C 571	18	0.9	498	10	ADQ93749	Adq93749 E. faeciu	C 644	18	0.9	622	4	AAV20340	Aav20340 Human bre
C 572	18	0.9	503	5	ABV60802	Abv60802 Human pro	C 645	18	0.9	622	4	AAV20340	Aav20340 Human bre
573	18	0.9	503	5	ADL40312	Adl40312 Human ova	C 646	18	0.9	624	6	ABT05956	Abt05956 Human pro
574	18	0.9	503	5	ADL40373	Adl40373 Human ova	C 647	18	0.9	625	5	ADL36444	Adl36444 Human ova
575	18	0.9	504	5	ADL40374	Adl40374 Human ova	648	18	0.9	625	5	ADL36444	Adl36444 Human ova
576	18	0.9	504	5	ADL39680	Adl39680 Human ova	649	18	0.9	629	5	ADL42828	Adl42828 Human ova
577	18	0.9	505	6	ABQ15474	Abq15474 Oligonuc	C 650	18	0.9	631	6	ADL11063	Adl11063 Human bre
C 578	18	0.9	505	6	AAH81430	Aah81430 Human ova	C 651	18	0.9	631	6	ADL11063	Adl11063 Human bre
C 579	18	0.9	508	5	AAH81430	Aah81430 Human ova	C 652	18	0.9	635	4	AAK67986	Aak67986 Human imm
C 580	18	0.9	510	6	ABQ30058	Abq30058 Oligonuc	C 653	18	0.9	635	5	AAH83399	Aah83399 Human ova
C 581	18	0.9	510	6	ABQ30059	Abq30059 Oligonuc	C 654	18	0.9	637	9	ACL15405	ACL15405 DNA clone
C 582	18	0.9	510	13	ACN45896	Acn45896 Cotton pr	C 655	18	0.9	637	9	ACL15405	ACL15405 DNA clone
C 583	18	0.9	511	5	ADL40384	Adl40384 Human ova	C 656	18	0.9	643	5	AAH83663	Aah83663 Human ova
C 584	18	0.9	513	5	AAH83810	Aah83810 Human ova	C 657	18	0.9	643	5	AAH83663	Aah83663 Human ova
585	18	0.9	514	5	AAH83810	Aah83810 Human ova	C 658	18	0.9	643	5	AAH83663	Aah83663 Human ova
586	18	0.9	518	13	ACN61295	Acn61295 Cotton gy	C 659	18	0.9	644	13	ACN54225	Acn54225 Cotton an
587	18	0.9	519	5	ADL36759	Adl36759 Human ova	C 660	18	0.9	650	5	AAV21829	Aav21829 Human col
588	18	0.9	519	5	ADI71603	Adi71603 Human ova	C 661	18	0.9	651	5	AAV21829	Aav21829 Human col
589	18	0.9	523	5	ADI75047	Adi75047 Human ova	C 662	18	0.9	651	5	AAV21829	Aav21829 Human col
590	18	0.9	523	5	ADI68685	Adi68685 Human ova	C 663	18	0.9	651	5	AAV21829	Aav21829 Human col
C 591	18	0.9	523	6	ABT05955	Abt05955 Human pro	C 664	18	0.9	651	5	AAV21829	Aav21829 Human col
C 592	18	0.9	527	8	ABZ72991	Abz72991 Rice leaf	C 665	18	0.9	666	5	AAV21829	Aav21829 Human col
C 593	18	0.9	531	5	ABV39452	Abv39452 Human pro	C 666	18	0.9	669	4	AAV21829	Aav21829 Human col
594	18	0.9	531	5	ABV45330	Abv45330 Human pro	C 667	18	0.9	677	6	AAV21829	Aav21829 Human col
595	18	0.9	531	5	ABV40866	Abv40866 Human pro	C 668	18	0.9	681	5	ABV22586	Abv22586 Human pro
596	18	0.9	531	5	ABV30479	Abv30479 Human pro	669	18	0.9	681	5	ABV22586	Abv22586 Human pro
597	18	0.9	531	5	ABV39429	Abv39429 Human pro	670	18	0.9	681	5	ABV22586	Abv22586 Human pro
C 598	18	0.9	533	13	ADQ51434	Adq51434 Novel can	671	18	0.9	681	5	ABV22586	Abv22586 Human pro
599	18	0.9	535	5	ADL39493	Adl39493 Human ova	672	18	0.9	681	5	ABV22586	Abv22586 Human pro
600	18	0.9	540	5	ABV58372	Abv58372 Human ova	673	18	0.9	681	5	ABV22586	Abv22586 Human pro
601	18	0.9	542	5	ADL40305	Adl40305 Human ova	674	18	0.9	681	5	ABV22586	Abv22586 Human pro
602	18	0.9	549	5	ADL39489	Adl39489 Human ova	675	18	0.9	681	5	ABV22586	Abv22586 Human pro
603	18	0.9	555	10	ABX05780	Abx05780 S. pneumo	676	18	0.9	681	5	ABV22586	Abv22586 Human pro
604	18	0.9	557	5	ABV32431	Abv32431 Human pro	677	18	0.9	681	5	ABV22586	Abv22586 Human pro

678	18	0.9	681	5	ABV29033	Human pro	Abv29033	Human pro	18	0.9	1141	10	ADC87248	Human GPC
679	18	0.9	681	5	ABV23138	Human pro	Abv23138	Human pro	18	0.9	1170	13	ADR73684	Rice prom
680	18	0.9	681	5	ABV25962	Human pro	Abv25962	Human pro	18	0.9	1185	6	ABQ44170	Oligonucle
681	18	0.9	681	5	ABV22471	Human pro	Abv22471	Human pro	18	0.9	1185	6	ABQ44171	Oligonucle
682	18	0.9	681	5	ABV24041	Human pro	Abv24041	Human pro	18	0.9	1221	3	AAC47697	Arabidops
683	18	0.9	681	5	ABV28979	Human pro	Abv28979	Human pro	18	0.9	1232	2	AZ16418	Human gen
684	18	0.9	681	5	ABV28286	Human pro	Abv28286	Human pro	18	0.9	1243	13	ADR73662	Rice prom
685	18	0.9	681	5	ABV28406	Human pro	Abv28406	Human pro	18	0.9	1262	2	AAX84980	Human sec
686	18	0.9	681	5	ABV20989	Human pro	Abv20989	Human pro	18	0.9	1262	8	ACD18906	Novel hum
687	18	0.9	681	5	ABV25977	Human pro	Abv25977	Human pro	18	0.9	1262	12	ADG78297	Human sec
688	18	0.9	681	5	ADL45505	Human ova	Adl45505	Human ova	18	0.9	1262	12	ADN60588	Human sec
689	18	0.9	684	3	AAA02603	Human col	Aaa02603	Human col	18	0.9	1288	3	AAC34972	Arabidops
690	18	0.9	689	6	ABQ37596	Oligonucle	Abq37596	Oligonucle	18	0.9	1318	6	AAS15009	Rice RecA
691	18	0.9	689	6	ABQ37597	Oligonucle	Abq37597	Oligonucle	18	0.9	1358	12	ADQ25247	Human sof
692	18	0.9	702	5	ADL40401	Human ova	Adl40401	Human ova	18	0.9	1358	12	ADQ25564	Human sof
693	18	0.9	705	5	ADL43058	Human ova	Adl43058	Human ova	18	0.9	1416	8	ABZ35906	Human sec
694	18	0.9	705	6	ABQ34131	Oligonucle	Abq34131	Oligonucle	18	0.9	1422	8	ABX72616	Human cdn
695	18	0.9	705	6	ABQ34130	Oligonucle	Abq34130	Oligonucle	18	0.9	1428	3	AAC33787	Arabidops
696	18	0.9	706	6	ABQ43116	Oligonucle	Abq43116	Oligonucle	18	0.9	1434	12	ADN10696	Nicotiana
697	18	0.9	706	6	ABQ43117	Oligonucle	Abq43117	Oligonucle	18	0.9	1449	13	ADT47611	Bacterial
698	18	0.9	709	6	ABQ46435	Oligonucle	Abq46435	Oligonucle	18	0.9	1464	8	ACA33146	Prokaryot
699	18	0.9	709	6	ABQ46434	Oligonucle	Abq46434	Oligonucle	18	0.9	1485	10	ADH84460	Enterococ
700	18	0.9	711	4	AAI97832	Human neu	Aai97832	Human neu	18	0.9	1496	2	AAQ72271	Rat MR77
701	18	0.9	714	4	ABL24699	Drosophil	Abi24699	Drosophil	18	0.9	1497	12	ADL16364	pBP118 ve
702	18	0.9	722	2	ADR02088	A. gossyp	Adr02088	A. gossyp	18	0.9	1511	6	ABQ14697	Oligonucle
703	18	0.9	727	2	ADR02319	A. gossyp	Adr02319	A. gossyp	18	0.9	1511	6	ABQ14696	Oligonucle
704	18	0.9	747	5	AA878273	DNA encod	Aas78273	DNA encod	18	0.9	1529	3	AAC54931	Arabidops
705	18	0.9	762	4	AAI21674	Human bre	Aai21674	Human bre	18	0.9	1537	3	AAC49912	Arabidops
706	18	0.9	794	5	ADL62414	Human ova	Adl62414	Human ova	18	0.9	1539	3	AAC53145	Arabidops
707	18	0.9	803	4	AA826758	Human gen	Aas26758	Human gen	18	0.9	1552	3	AAC40750	Arabidops
708	18	0.9	803	4	AA826761	Human gen	Aas26761	Human gen	18	0.9	1576	5	AAF24154	Human sec
709	18	0.9	803	8	ABX74110	Human nov	Abx74110	Human nov	18	0.9	1589	12	ADH18972	Human cel
710	18	0.9	803	8	ABX74107	Human nov	Abx74107	Human nov	18	0.9	1589	12	ADH18972	Human cel
711	18	0.9	816	13	ADR63888	Cotton cd	Adr63888	Cotton cd	18	0.9	1594	12	ADN10662	Nicotiana
712	18	0.9	824	6	ABX91971	Lung spec	Abx91971	Lung spec	18	0.9	1601	12	ADN10704	Nicotiana
713	18	0.9	833	3	AAC49657	Arabidops	Aac49657	Arabidops	18	0.9	1605	2	AAX200809	Human sec
714	18	0.9	848	6	ABQ30456	Oligonucle	Abq30456	Oligonucle	18	0.9	1610	12	ADN10642	Nicotiana
715	18	0.9	848	6	ABQ30457	Oligonucle	Abq30457	Oligonucle	18	0.9	1610	12	ADN10642	Nicotiana
716	18	0.9	850	6	ABQ48654	Oligonucle	Abq48654	Oligonucle	18	0.9	1623	12	ADN10600	Nicotiana
717	18	0.9	850	6	ABQ48655	Oligonucle	Abq48655	Oligonucle	18	0.9	1636	10	ADF08963	cdna enco
718	18	0.9	856	4	AA861013	Human can	Aas61013	Human can	18	0.9	1675	6	ABQ78825	Human Mch
719	18	0.9	872	6	ABQ45452	Oligonucle	Abq45452	Oligonucle	18	0.9	1679	6	AAL51168	Peroxidas
720	18	0.9	876	6	ABQ45453	Oligonucle	Abq45453	Oligonucle	18	0.9	1679	6	AAL51168	Peroxidas
721	18	0.9	878	6	ABQ35912	Oligonucle	Abq35912	Oligonucle	18	0.9	1704	3	AAC47127	Arabidops
722	18	0.9	878	6	ABQ35913	Oligonucle	Abq35913	Oligonucle	18	0.9	1704	3	AAC47127	Arabidops
723	18	0.9	882	6	ABN91503	Staphyloc	Abn91503	Staphyloc	18	0.9	1721	12	ADH41325	Human ova
724	18	0.9	882	13	ADS03045	Staphyloc	Ads03045	Staphyloc	18	0.9	1729	8	ACF62822	Colon can
725	18	0.9	887	2	AAZ96455	S. preumo	Aaz96455	S. preumo	18	0.9	1761	3	AAF70076	Human ova
726	18	0.9	898	4	AAI94177	Human neu	Aai94177	Human neu	18	0.9	1761	6	ABN72970	cdna sequ
727	18	0.9	904	4	AA822326	Human cdn	Aas22326	Human cdn	18	0.9	1761	9	ADA08540	Human ova
728	18	0.9	935	4	AAI10399	Human cdn	Aai10399	Human cdn	18	0.9	1761	10	ADF08883	cdna enco
729	18	0.9	949	3	AAA35137	Human ade	Aaa35137	Human ade	18	0.9	1761	2	AAX99572	Nucleic a
730	18	0.9	949	3	AAF21259	Human low	Aaf21259	Human low	18	0.9	1761	2	AAX99572	Nucleic a
731	18	0.9	949	10	ABZ96953	Human nuc	Abz96953	Human nuc	18	0.9	1783	4	AAS34928	cdna enco
732	18	0.9	949	11	ABD20802	Human pul	Abd20802	Human pul	18	0.9	1783	10	ADC46086	Human neo
733	18	0.9	971	11	ACN80598	Breast ca	Acn80598	Breast ca	18	0.9	1800	6	ABA04826	Human myo
734	18	0.9	972	13	ADC91448	E. faeciu	Adc91448	E. faeciu	18	0.9	1821	8	ACF73124	Staphyloc
735	18	0.9	992	13	ADS47792	Bacterial	Ads47792	Bacterial	18	0.9	1845	6	AD343318	Human PKI
736	18	0.9	1015	6	ABQ53075	Oligonucle	Abq53075	Oligonucle	18	0.9	1893	6	ABN70106	Streptococ
737	18	0.9	1015	6	ABQ53074	Oligonucle	Abq53074	Oligonucle	18	0.9	1941	6	ABQ54755	Human ova
738	18	0.9	1017	5	AA878120	DNA encod	Aas78120	DNA encod	18	0.9	1981	3	AAX250482	Corn sulp
739	18	0.9	1019	13	ADR64356	Cotton cd	Adr64356	Cotton cd	18	0.9	1995	6	ABL88382	Pain regu
740	18	0.9	1049	6	ABQ29059	Oligonucle	Abq29059	Oligonucle	18	0.9	2000	6	ABZ15902	Arabidops
741	18	0.9	1049	6	ABQ29058	Oligonucle	Abq29058	Oligonucle	18	0.9	2000	6	ABZ16643	Arabidops
742	18	0.9	1049	12	ADO02565	Soybean o	Ado02565	Soybean o	18	0.9	2000	6	ABZ15449	Arabidops
743	18	0.9	1049	13	ADI42014	Plant tra	Adi42014	Plant tra	18	0.9	2000	8	ADA72730	Rice gene
744	18	0.9	1059	10	ACF71850	Phororhab	Acf71850	Phororhab	18	0.9	2000	8	ADA72196	Rice gene
745	18	0.9	1060	6	ADN73046	cdna sequ	Adn73046	cdna sequ	18	0.9	2000	8	ADA71873	Rice gene
746	18	0.9	1060	9	ADA08721	Human O77	Ada08721	Human O77	18	0.9	2000	10	ACC60882	Gene sequ
747	18	0.9	1060	10	ADF09064	cdna enco	Adf09064	cdna enco	18	0.9	2000	10	ADK62281	Disease t
748	18	0.9	1071	5	AA888100	Human FLE	Aac88100	Human FLE	18	0.9	2000	12	ADJ41413	Plant CDN
749	18	0.9	1074	3	AAZ52291	Maize rep	Aaz52291	Maize rep	18	0.9	2012	12	ADO21867	Human ves
750	18	0.9	1120	1	AAN70643	Cyclohexi	Aan70643	Cyclohexi	18	0.9	2017	2	AAT60713	Saccharom

824	18	0.9	2059	8	ABX95379	Abx95379 S. pneumoniae	897	18	0.9	2957	2	AAV18462	Aav18462 Human gra
825	18	0.9	2070	12	ADL16362	Adl16362 pBP116 ve	c 898	18	0.9	2957	5	AAS92281	Aas92281 DNA encod
c 826	18	0.9	2084	12	ADQ24447	Adq24447 Human sof	c 899	18	0.9	2996	3	AAA70001	Aaa70001 Human ova
c 827	18	0.9	2090	11	ADI30900	Adi30900 Human cdn	900	18	0.9	2996	4	AAS55680	Aas55680 Human ova
c 828	18	0.9	2108	10	ADA52503	Ada52503 Human cod	901	18	0.9	2996	6	ABN72895	Abn72895 Full leng
c 829	18	0.9	2121	8	ABZ74640	Abz74640 Secreted	902	18	0.9	2996	6	ABN72974	Abn72974 Hypocheti
c 830	18	0.9	2121	8	ADA44569	Ada44569 Human sec	903	18	0.9	2996	9	ADA09060	Ada09060 Human ova
c 831	18	0.9	2121	12	ADN41709	Adn41709 Novel hum	904	18	0.9	2996	9	ADA08615	Ada08615 Human O77
c 832	18	0.9	2122	8	ABZ74641	Abz74641 Secreted	905	18	0.9	2996	10	ADF08807	Adf08807 CDNA enco
c 833	18	0.9	2122	8	ADA44570	Ada44570 Human sec	906	18	0.9	2996	10	ADF08958	Adf08958 CDNA enco
c 834	18	0.9	2125	10	ACC72758	Acc72758 Human can	907	18	0.9	2996	10	ADA65555	Ada65555 Human ova
c 835	18	0.9	2136	10	ADH84180	Adh84180 Enterococ	908	18	0.9	2996	12	ADN40450	Adn40450 Human bre
c 836	18	0.9	2136	8	ABX63197	Abx63197 Human cdn	c 909	18	0.9	3002	4	ABL21372	AbL21372 Drosophil
c 837	18	0.9	2225	10	ADB62343	Adb62343 Human cdn	c 910	18	0.9	3007	13	ADR07533	Adr07533 Full leng
838	18	0.9	2284	4	ABL21228	AbL21228 Drosophil	911	18	0.9	3015	4	AAH54037	Aah54037 S. epider
839	18	0.9	2289	12	ADL16354	Adl16354 pBP109 ex	912	18	0.9	3060	4	AAF77098	Aaf77098 Arabidops
c 840	18	0.9	2308	12	ADO21866	Ado21866 Human ves	913	18	0.9	3060	10	ACF35553	Acf35553 Arabidops
c 841	18	0.9	2314	6	ABK84154	Abk84154 Human cdn	914	18	0.9	3075	12	ADO33502	Ado33502 Novel mou
c 842	18	0.9	2318	3	AAC59907	Aac59907 Human sec	915	18	0.9	3086	6	ABS66329	Abs66329 Soybean l
843	18	0.9	2318	8	ABZ73286	Abz73286 Secreted	c 916	18	0.9	3110	2	AAT84234	Aat84234 DNA encod
844	18	0.9	2318	10	ADC20067	Adc20067 Human sec	c 917	18	0.9	3110	2	AAV53557	Aav53557 DNA encod
845	18	0.9	2318	10	ABT16764	Abt16764 Human sec	c 918	18	0.9	3114	6	ABS66336	Abs66336 Soybean l
846	18	0.9	2318	10	ABZ66897	Abz66897 Human sec	c 919	18	0.9	3115	13	ADR23587	Adr23587 Brestet ca
c 847	18	0.9	2319	10	ADT57341	Adt57341 Human cel	c 920	18	0.9	3157	4	AAS36928	Aas36928 Human car
c 848	18	0.9	2333	13	ADT66713	Adt66713 Human CDC	c 921	18	0.9	3157	13	ADJ09040	Adj09040 Human car
c 849	18	0.9	2337	12	ADL16340	Adl16340 Bacillus	c 922	18	0.9	3169	10	AAS36929	Aas36929 Human car
850	18	0.9	2344	5	AAS66472	Aas66472 DNA encod	c 923	18	0.9	3169	10	ADE47623	Ade47623 Human car
851	18	0.9	2396	10	ACF58208	Acf58208 B. anthrac	c 924	18	0.9	3169	13	ADJ09041	Adj09041 Human car
c 852	18	0.9	2415	4	AAI98104	Aai98104 Human neu	c 925	18	0.9	3176	3	AACT76094	Aac76094 Human ORF
c 853	18	0.9	2422	6	AAI37665	Aai37665 Human G-P	c 926	18	0.9	3188	6	ABL61777	AbL61777 Colon ade
c 854	18	0.9	2430	4	AAC86015	Aac86015 Wild type	927	18	0.9	3188	9	ACC85162	Acc85162 Human P13
855	18	0.9	2449	11	ADM01613	Adm01613 Human cdn	928	18	0.9	3188	10	ADD29777	Add29777 Human tum
c 856	18	0.9	2481	4	AAH26415	Aah26415 Arancicola	929	18	0.9	3188	2	AAZ11494	Aaz11494 Human pro
c 857	18	0.9	2481	9	ADA09915	Ada09915 Human rec	c 930	18	0.9	3190	12	ADO335413	Ado335413 Novel mou
c 858	18	0.9	2489	2	AAZ31960	Aaz31960 S. pneumo	c 931	18	0.9	3201	8	ABX95377	Abx95377 DNA encod
c 859	18	0.9	2512	4	ABL22466	AbL22466 Drosophil	932	18	0.9	3222	8	AAQ70179	Aaq70179 Sequence
c 860	18	0.9	2533	2	AAI13589	Aai13589 Enterococ	933	18	0.9	3294	2	AAQ70179	Aaq70179 Sequence
c 861	18	0.9	2533	6	ABS93384	Abs93384 Enterococ	934	18	0.9	3298	5	ABV25485	Abv25485 Human pro
c 862	18	0.9	2537	4	ABL21768	AbL21768 Drosophil	c 935	18	0.9	3323	4	ABL15666	AbL15666 Drosophil
c 863	18	0.9	2544	4	ABL09232	AbL09232 Drosophil	c 936	18	0.9	3400	2	AAO20297	Aao20297 Human IL-
c 864	18	0.9	2560	6	ABN59748	Abn59748 Novel hum	c 937	18	0.9	3418	4	ABL02858	AbL02858 Drosophil
c 865	18	0.9	2574	11	ADM01989	Adm01989 Human cdn	c 938	18	0.9	3447	6	ABN72972	Abn72972 Truncated
c 866	18	0.9	2608	3	AAZ70075	Aaz70075 Human ova	939	18	0.9	3447	9	ADA08609	Ada08609 Human O77
c 867	18	0.9	2608	9	ADN72969	Adn72969 cDNA sequ	940	18	0.9	3447	10	ADF08952	Adf08952 CDNA enco
c 868	18	0.9	2608	9	ADA08539	Ada08539 Human ova	941	18	0.9	3447	10	ADG46239	Adg46239 Human ova
c 869	18	0.9	2608	10	ADF08882	Adf08882 CDNA enco	942	18	0.9	3463	2	AAZ61728	Aaz61728 Streptoco
c 870	18	0.9	2608	10	ADG46169	Adg46169 Human ova	943	18	0.9	3463	2	AAZ61728	Aaz61728 Streptoco
c 871	18	0.9	2611	6	ABZ70189	Abz70189 Ribosomal	944	18	0.9	3467	13	ADR06673	Adr06673 Full leng
c 872	18	0.9	2622	4	ABK42633	Abk42633 Genomic s	c 945	18	0.9	3521	4	ABL05022	AbL05022 Drosophil
c 873	18	0.9	2622	5	ABA20094	AbA20094 Human ner	c 946	18	0.9	3529	4	ABL05022	AbL05022 Drosophil
c 874	18	0.9	2622	9	ADB60789	Adb60789 Connectiv	947	18	0.9	3546	8	ABX05223	Abx05223 Human nov
c 875	18	0.9	2638	4	AAC84370	Aac84370 Mouse Zac	948	18	0.9	3557	4	AAH18639	Aah18639 Human cdn
c 876	18	0.9	2638	10	ABX93337	Abx93337 CDNA enco	949	18	0.9	3557	5	ABA83109	AbA83109 HOST-1 ov
c 877	18	0.9	2686	2	AAV82457	Aav82457 Recombina	950	18	0.9	3557	6	ABN72973	Abn72973 Full nucl
c 878	18	0.9	2703	4	ABL11944	AbL11944 Drosophil	951	18	0.9	3557	6	ABN72975	Abn72975 cDNA sequ
c 879	18	0.9	2720	12	ADQ24606	Adq24606 Human sof	952	18	0.9	3557	9	ADA08616	Ada08616 Human CDN
c 880	18	0.9	2720	12	ADQ24903	Adq24903 Human sof	953	18	0.9	3557	9	ADF08953	Adf08953 CDNA enco
c 881	18	0.9	2720	12	ADQ24903	Adq24903 Human sof	954	18	0.9	3557	10	ADF08953	Adf08953 CDNA enco
c 882	18	0.9	2779	4	ABL24698	AbL24698 Drosophil	955	18	0.9	3557	10	ADF08959	Adf08959 Human ova
c 883	18	0.9	2796	2	AAV82472	Aav82472 Recombina	956	18	0.9	3557	10	ADG46240	Adg46240 Human col
c 884	18	0.9	2800	4	ABL22214	AbL22214 Drosophil	957	18	0.9	3557	12	ADQ08770	Adq08770 Human ova
c 885	18	0.9	2851	13	ADR08132	Adr08132 Full leng	958	18	0.9	3557	12	ADQ29638	Adq29638 Human col
c 886	18	0.9	2901	4	AAH54046	Aah54046 S. epider	959	18	0.9	3559	11	ADM30753	Adm30753 Human can
c 887	18	0.9	2903	5	AAS78152	Aas78152 DNA encod	c 960	18	0.9	3584	4	ABL41462	AbL41462 Drosophil
c 888	18	0.9	2932	8	ABZ10173	AbZ10173 Haematopo	c 961	18	0.9	3584	4	ABL41462	AbL41462 Drosophil
c 889	18	0.9	2932	10	ADB54205	AdB54205 Pretreate	962	18	0.9	3596	4	ABL27422	AbL27422 Drosophil
c 890	18	0.9	2932	10	ADB84141	AdB84141 Human lym	963	18	0.9	3596	4	ABL27422	AbL27422 Drosophil
c 891	18	0.9	2932	13	ADS89505	Ads89505 Oligonucle	964	18	0.9	3600	11	ACN91879	Acn91879 Brestet ca
c 892	18	0.9	2943	3	AAA70074	Aaa70074 Human ova	c 965	18	0.9	3613	13	ADR08401	Adr08401 Full leng
c 893	18	0.9	2943	6	ABN72968	Abn72968 CDNA sequ	966	18	0.9	3631	12	ADL72876	AdL72876 Anthrax v
c 894	18	0.9	2943	10	ADA08538	Ada08538 Human ova	967	18	0.9	3631	12	ADL72876	AdL72876 Anthrax v
c 895	18	0.9	2943	10	ADF08881	Adf08881 CDNA enco	968	18	0.9	3694	4	ABL21736	AbL21736 Drosophil
c 896	18	0.9	2943	10	ADG46168	Adg46168 Human ova	c 969	18	0.9	3720	6	AAZ27687	Aaz27687 Plasmid p
c 897	18	0.9	2949	4	ABL23052	AbL23052 Drosophil	c 970	18	0.9	3732	4	ABL03714	AbL03714 Drosophil

AB210934	Drosophil	18	0.9	3732	4	ABL20934
ADQ24115	Human sof	18	0.9	3738	12	ADQ24115
ADQ64985	Novel hum	18	0.9	3743	12	ADQ64985
ABX08985	cdNA enco	18	0.9	3798	18	ABX08985
AAX28141	CCOAWT p	18	0.9	3800	2	AAX28141
Aaz60808	Nucleotid	18	0.9	3800	3	Aaz60808
Aah54069	S. epider	18	0.9	3835	4	Aah54069
ADR41249	Human CD-	18	0.9	3892	7	ADR41249
Adr06677	Full leng	18	0.9	3901	13	ADR06677
Adq08599	Ciona int	18	0.9	3914	12	ADQ08599
Aaz34950	Human ade	18	0.9	3929	3	Aaz34950
Aaf21072	Human low	18	0.9	3929	3	Aaf21072
Abz296766	Human nuc	18	0.9	3929	10	ABZ296766
ABD20615	Human pul	18	0.9	3929	11	ABD20615
Aan90569	Ovine Y-c	18	0.9	3983	1	AAN90569
Aah54621	S. epider	18	0.9	3993	4	Aah54621
Ades89768	Oligonucl	18	0.9	4001	13	ADes89768
Aas83954	DNA encod	18	0.9	4083	5	AAS83954
ABZ10055	Haematopo	18	0.9	4110	8	ABZ10055
ABK64835	Human ben	18	0.9	4148	6	ABK64835
Adf09649	Human exp	18	0.9	4148	10	ADF09649
ACn37699	Tumour-ab	18	0.9	4148	13	ACN37699
ADR08234	Full leng	18	0.9	4184	13	ADR08234
ADL62845	Human ova	18	0.9	4209	5	ADL62845
ADs46785	Bacterial	18	0.9	4224	13	ADs46785
Aaf18289	Lung canc	18	0.9	4253	3	AAF18289
ACA52686	Prokaryot	18	0.9	4305	8	ACA52686
ABL09288	Drosophil	18	0.9	4453	4	ABL09288
AKK69549	Human imm	18	0.9	4458	4	AKK69549
ADH41327	Human ova	18	0.9	4494	12	ADH41327
Aaf55367	Nucleotid	18	0.9	4497	4	Aaf55367

ABZ75215	standard; cdNA; 2030 BP.
ABZ75215	
ABZ75215	
23-APR-2003	(first entry)
Arabidopsis thaliana endomembrane associated promoter cdNA.	
ENDO; endomembrane associated; promoter; expression; gene; ss.	
Arabidopsis thaliana.	
OS	
WO200268665-A2.	
06-SEP-2002.	
14-FEB-2002; 2002WO-EP002894.	
22-FEB-2001; 2001US-0270779P.	
(RHOB-) RHOBIO.	
Thomas T, Nuccio M, Hsieh T;	
WPI; 2002-707007/76.	
New isolated ENDO promoter from the gene of Arabidopsis thaliana, useful for directing expression of genes in plants.	
Claim 1; Page 17; 18pp; English.	
The invention relates to the novel isolated Arabidopsis thaliana endomembrane associated (ENDO) gene promoter sequence. The nucleic acid is useful for directing expression of genes in plants. The present sequence represents the A. thaliana ENDO promoter of the invention	

XX	Sequence 2030 BP; 722 A; 287 C; 319 G; 702 T; 0 U; 0 Other;
SQ	
Query Match	100.0%; Score 2030; DB 6; Length 2030;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 2030; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTTCTAGAAGGATGGACCAATTGAAGAATACTTTCTCTTTTCTATTTTATTTTATTTAGATTAG 60
DB	1 CTTCTAGAAGGATGGACCAATTGAAGAATACTTTCTCTTTTCTATTTTATTTTATTTAGATTAG 60
QY	61 AAAATCATATTCATTACAAAAGGAAAAAATAATTTTCTATCTCTAAAGTTATAAC 120
DB	61 AAAATCATATTCATTACAAAAGGAAAAAATAATTTTCTATCTCTAAAGTTATAAC 120
QY	121 TTACAATTTTCCACACTTCAGTTGGTAGTATTAAATTTATCTATTTTATCAAAAGTTTGG 180
DB	121 TTACAATTTTCCACACTTCAGTTGGTAGTATTAAATTTATCTATTTTATCAAAAGTTTGG 180
QY	181 TTTTAGGAAAAATGTATCTTTTCATATAAAAAATATATAGATCTTCAAGAAACTGAATTT 240
DB	181 TTTTAGGAAAAATGTATCTTTTCATATAAAAAATATATAGATCTTCAAGAAACTGAATTT 240
QY	241 GGGTTTTCAACTATTTTATCGTTTGACACTACTTTGACACTTATCAAAAAGAGTTCAAATA 300
DB	241 GGGTTTTCAACTATTTTATCGTTTGACACTACTTTGACACTTATCAAAAAGAGTTCAAATA 300
QY	301 GAAAAATAGAATCGAATCACACGTTTCAGTGTGAAGAGGATTTTGATATTCGTCGACATTT 360
DB	301 GAAAAATAGAATCGAATCACACGTTTCAGTGTGAAGAGGATTTTGATATTCGTCGACATTT 360
QY	361 TAAAGAGTGTGTTTTGTTTTTTTTTCCAAATCTGCATGGTTTTTTCGTTCCGTTGAACCAAAAT 420
DB	361 TAAAGAGTGTGTTTTGTTTTTTTTTCCAAATCTGCATGGTTTTTTCGTTCCGTTGAACCAAAAT 420
QY	421 TCAACACTTTGTATAAACCGAATAGTAATATATCTAGACGTACGCCAATACCAAAAATAAAA 480
DB	421 TCAACACTTTGTATAAACCGAATAGTAATATATCTAGACGTACGCCAATACCAAAAATAAAA 480
QY	481 ATTTAAACTCAATTCACAAATTTGAATCTACACCATATCATGCATATATATCAGCAACTTA 540
DB	481 ATTTAAACTCAATTCACAAATTTGAATCTACACCATATCATGCATATATATCAGCAACTTA 540
QY	541 GAATAATCAATGAAATTTAATCGAGGATAATCAATATCCAACCTCAACGATAATCAAAAGC 600
DB	541 GAATAATCAATGAAATTTAATCGAGGATAATCAATATCCAACCTCAACGATAATCAAAAGC 600
QY	601 CTAATAATAGATCAATGAAATCAAAATACTAAACATAGTAATATACATTTGATTGTGTTA 660
DB	601 CTAATAATAGATCAATGAAATCAAAATACTAAACATAGTAATATACATTTGATTGTGTTA 660
QY	661 AACAGAAATATACATTTATGAATGAAATATGAATATGAATATGAATATGAATATGAATATGA 720
DB	661 AACAGAAATATACATTTATGAATGAAATATGAATATGAATATGAATATGAATATGAATATGA 720
QY	721 TATGTTACAACCTACAGATCACCATCCACAATTAACAAATCCGATTTGGTGCGGGCCATTGTT 780
DB	721 TATGTTACAACCTACAGATCACCATCCACAATTAACAAATCCGATTTGGTGCGGGCCATTGTT 780
QY	781 TCGATATTTTGCCAAATCTGTG

Db 961 CTTTCATGTCGACGTAACAAGACTTATTTTCCGGTTGAAATTTGGTTAACTATTGAGATT 1020  
Qy 1021 GTGCTAACCGAAAAACAGAAACGGTTATGACGCCAACAGAGGCAAGAGGGGTAAAAACGAGAA 1080  
Db 1021 GTGCTAACCGAAAAACAGAAACGGTTATGACGCCAACAGAGGCAAGAGGGGTAAAAACGAGAA 1080  
Qy 1081 AGAGGGGATGGCAGAAATCGTAATTAACAAGGAAATAAAGGGTGGTTTCACGATAAGTC 1140  
Db 1081 AGAGGGGATGGCAGAAATCGTAATTAACAAGGAAATAAAGGGTGGTTTCACGATAAGTC 1140  
Qy 1141 TGTCTATATGACGCGAAAGGGTTTCTTAAATTCAGAGACAAATTAATCAGTTTCGTGTG 1200  
Db 1141 TGTCTATATGACGCGAAAGGGTTTCTTAAATTCAGAGACAAATTAATCAGTTTCGTGTG 1200  
Qy 1201 TTTGGAGAAGAAGAACAGATCAATACGAGGAGAGATCTCTAAAGAGATTTATCGTT 1260  
Db 1201 TTTGGAGAAGAAGAACAGATCAATACGAGGAGAGATCTCTAAAGAGATTTATCGTT 1260  
Qy 1261 TCAAGTAAGTCTCTTTATCAAACTCTTAATATAAACAATCAAAACATGAACACGTCGTG 1320  
Db 1261 TCAAGTAAGTCTCTTTATCAAACTCTTAATATAAACAATCAAAACATGAACACGTCGTG 1320  
Qy 1321 TCTTCGTTTCGATCTAGATACGATTTTTCATGTGAATGAATCTCTGTTTATATAC 1380  
Db 1321 TCTTCGTTTCGATCTAGATACGATTTTTCATGTGAATGAATCTCTGTTTATATAC 1380  
Qy 1381 TACTAGGTTGTTCAATATATTTTCCGAGAAATACAGAGGAAACAAAGTTAGTGAATATAT 1440  
Db 1381 TACTAGGTTGTTCAATATATTTTCCGAGAAATACAGAGGAAACAAAGTTAGTGAATATAT 1440  
Qy 1441 TGAATCAGAGTATGAATATATATACATAAATCATGTTTCTCTCAAGCATCTACGT 1500  
Db 1441 TGAATCAGAGTATGAATATATATACATAAATCATGTTTCTCTCAAGCATCTACGT 1500  
Qy 1501 TGAATATATATGAAGATTTTTCGTTGTAAGAAATATGTATGAGAAGTTTCATCTTC 1560  
Db 1501 TGAATATATATGAAGATTTTTCGTTGTAAGAAATATGTATGAGAAGTTTCATCTTC 1560  
Qy 1561 ATAATAGTGAACAACTCTCTTTATACCAAAAAAATTTGAAAAAATTTAGTGAAA 1620  
Db 1561 ATAATAGTGAACAACTCTCTTTATACCAAAAAAATTTGAAAAAATTTAGTGAAA 1620  
Qy 1621 CTCTCTTGTCCGATAGGTTAGGTTGGACTCAGAAATCAAAATACGATTAGCATACAA 1680  
Db 1621 CTCTCTTGTCCGATAGGTTAGGTTGGACTCAGAAATCAAAATACGATTAGCATACAA 1680  
Qy 1681 ATTTTGTGGCATGCAATTTATGTCGAGGTAAATATATACCAATAGAAACATATTTTA 1740  
Db 1681 ATTTTGTGGCATGCAATTTATGTCGAGGTAAATATATATACCAATAGAAACATATTTTA 1740  
Qy 1741 GAGTAGTTAAGATTATGATGAAGAAATCTATTACGATAAGCATAAATTTTCTTTTG 1800  
Db 1741 GAGTAGTTAAGATTATGATGAAGAAATCTATTACGATAAGCATAAATTTTCTTTTG 1800  
Qy 1801 CTGTTCTTGTGTTTGTGCTTTTATAGAAATGATGATGCTTTTGTGTTTTCAC 1860  
Db 1801 CTGTTCTTGTGTTTGTGCTTTTATAGAAATGATGATGCTTTTGTGTTTTCAC 1860  
Qy 1861 AGTAGATGCTACTATACACATACATGAGTAAAGTGGTAGTTTATATAGAGAGATTGA 1920  
Db 1861 AGTAGATGCTACTATACACATACATGAGTAAAGTGGTAGTTTATATAGAGAGATTGA 1920  
Qy 1921 TTTTTCGTATATTTCTTTTGTGAAAAATAATATGCTGTAATAATTTATGTTTATTAATTT 1980  
Db 1921 TTTTTCGTATATTTCTTTTGTGAAAAATAATATGCTGTAATAATTTATGTTTATTAATTT 1980  
Qy 1981 GACAGATTGTTTACGTTGAGAAGTTTAAATTTAGATTAAACACAAAAAG 2030  
Db 1981 GACAGATTGTTTACGTTGAGAAGTTTAAATTTAGATTAAACACAAAAAG 2030

ABZ75216 standard; cDNA; 2042 BP.  
XX  
AC ABZ75216;  
XX  
DT 23-APR-2003 (first entry)  
XX  
DE Arabidopsis thaliana RC15 clone promoter fragment cDNA.  
XX  
KW ENDO; endomembrane associated; promoter; expression; gene; RC15; ss.  
XX  
OS Arabidopsis thaliana.  
OS Synthetic.  
PN W0200268665-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 14-FEB-2002; 2002WO-EP002894.  
XX  
PR 22-FEB-2001; 2001US-0270779P.  
XX  
PA (RHOB-) RHOBIO.  
XX  
PI Thomas T, Nuccio M, Hsieh T;  
XX  
DR WPI; 2002-707007/76.  
XX  
PT New isolated ENDO promoter from the gene of Arabidopsis thaliana, useful  
PT for directing expression of genes in plants.  
XX  
PS Example 1; Page 18; 18pp; English.  
XX  
CC The invention relates to the novel isolated Arabidopsis thaliana  
CC endomembrane associated (ENDO) gene promoter sequence. The nucleic acid  
CC is useful for directing expression of genes in plants. The present  
CC sequence represents the promoter fragment taken from A. thaliana clone  
CC RC15  
XX  
SQ Sequence 2042 BP; 725 A; 290 C; 322 G; 705 T; 0 U; 0 Other;  
Query Match 100.0%; Score 2030; DB 6; Length 2042;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTTCTAGAGGATGGACCATTCGAAGAATACCTTTCTCTTTCTATTATTTTGAATTAG 60  
Db 7 CTTCTAGAGGATGGACCATTCGAAGAATACCTTTCTCTTTCTATTATTTTGAATTAG 66  
Qy 61 AAAATCATATTTCAATTACAAAAGGAAAAAATAATTTTGTATCTCTAAAGTTATAAC 120  
Db 67 AAAATCATATTTCAATTACAAAAGGAAAAAATAATTTTGTATCTCTAAAGTTATAAC 126  
Qy 121 TTACAATTTTCCACACTTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAAGTTGG 180  
Db 127 TTACAATTTTCCACACTTCAGTTTGGTAGTATTAATTTATCTATTTTATCAAAGTTGG 186  
Qy 181 TTTTGGAAAAATGATCTTTTCATATAAAAAATATATAGATCTTCAAAGAACTGAATT 240  
Db 187 TTTTGGAAAAATGATCTTTTCATATAAAAAATATATAGATCTTCAAAGAACTGAATT 246  
Qy 241 GGGTTTTCACACTATTTTATCGTTTGGACACTACTTTGACTTTATCAAAAAGAGTTCAAAATA 300  
Db 247 GGGTTTTCACACTATTTTATCGTTTGGACACTACTTTGACTTTATCAAAAAGAGTTCAAAATA 306  
Qy 301 GAAAAATAGAAATCGAATCAACAGTTTTCAGTGTGAAGGGGATTTGATATTGGTGCACATTT 360  
Db 307 GAAAAATAGAAATCGAATCAACAGTTTTCAGTGTGAAGGGGATTTGATATTGGTGCACATTT 366  
Qy 361 TAAAGAGTTGTTTGTGTTTTCCTTTCCTGATGTTTTCCTGTTGAAACCAAT 420  
Db 367 TAAAGAGTTGTTTGTGTTTTCCTTTCCTGATGTTTTCCTGTTGAAACCAAT 426  
Qy 421 TCAACACTTTGTATAAAAACCGAATAGTAAATATATAGACGTACGCCAATACCAAAAATAA 480



|||||  
427 TCACACATTTGTATATAACCGAATAGTAATATACTAGACGTAGCCGATACCAAAATAATA 486  
QY |||||  
481 ATTAATACTCAATTCACAAATTGAATCTACACATATCATCATATATATATACGACCACTTA 540  
D |||||  
487 ATTAATACTCAATTCACAAATTGAATCTACACATATCATCATATATATATACGACCACTTA 546  
QY |||||  
541 GAATAATCAATGAAATTTAATCGAGATTAATCAATATCCAATCTCAACGATTAATCAAAAGC 600  
D |||||  
547 GAATAATCAATGAAATTTAATCGAGATTAATCAATATCCAATCTCAACGATTAATCAAAAGC 606  
QY |||||  
601 CTAATAATAGATCAATGAAATCAAAATACTAAACATAGTAATAATACATTTGTTGTTA 660  
D |||||  
607 CTAATAATAGATCAATGAAATCAAAATACTAAACATAGTAATAATACATTTGTTGTTA 666  
QY |||||  
661 AACAGAAATTAATACATTTAATAGTATGAAATATGAATATAAATAGAGACGCTTA 720  
D |||||  
667 AACAGAAATTAATACATTTAATAGTATGAAATATGAATATAAATAGAGACGCTTA 726  
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721 TATGTTTACAATACAGATCACCATCCACAATTAACAATCCGATTTGGTGGGGCCATTGTT 780  
D |||||  
727 TATGTTTACAATACAGATCACCATCCACAATTAACAATCCGATTTGGTGGGGCCATTGTT 786  
QY |||||  
781 TCGATATTTGCCAACTGTGATGATGTGACTGCGACTGGCATATTTTCCCTCTCTGATT 840  
D |||||  
787 TCGATATTTGCCAACTGTGATGATGTGACTGCGACTGGCATATTTTCCCTCTCTGATT 846  
QY |||||  
841 ACGTTTTTACCCTTTCCCTCTCTGTTTTACCGTTAATCAATTTTACTATTTGTACCGCT 900  
D |||||  
847 ACGTTTTTACCCTTTCCCTCTCTGTTTTACCGTTAATCAATTTTACTATTTGTACCGCT 906  
QY |||||  
901 GTCTTTTACCTTTTAAAGAAACCCAAACCCGAAATCATACTATACCGAAATCACATGT 960  
D |||||  
907 GTCTTTTACCTTTTAAAGAAACCCAAACCCGAAATCATACTATACCGAAATCACATGT 966  
QY |||||  
961 CTTTCATGTTGACGTAAACAAGACTTATTTTCCGGTTGAAATTTGGTTTAACTATTGAGATT 1020  
D |||||  
967 CTTTCATGTTGACGTAAACAAGACTTATTTTCCGGTTGAAATTTGGTTTAACTATTGAGATT 1026  
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1021 GTGCTAACCGAAAAACAGAAACCGTTATGACGCCAACGAGGCAAGGGGTAAAAACGAGAA 1080  
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RESULT 3  
ABZ16347  
ID ABZ16347 standard; DNA; 1064 BP.

XX ABZ16347;

XX DT 21-JAN-2003 (first entry)

XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4152.

XX XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX OS Arabidopsis thaliana.

XX PN WO200216655-A2.

XX PD 28-FEB-2002.

XX PF 24-AUG-2001; 2001WO-US026685.

XX PR 24-AUG-2000; 2000US-0227866P.

XX PR 26-JAN-2001; 2001US-0264647P.

XX PR 22-JUN-2001; 2001US-0300111P.

XX (SCRI ) SCRIPPS RES INST.

XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX PI Harper JF, Kreps J, Wang X, Zhu T;

XX DR WPI; 2002-304127/34.

XX PT Identifying a stress condition to which a plant cell has been exposed and

XX PT producing plants with increased tolerance to these abiotic stresses.

XX PS Claim 144; SEQ ID NO 4152; 577pp + Sequence Listing; English.

XX CC The invention relates to identifying a stress condition to which a plant

CC cell has been exposed, comprising: (a) contacting nucleic acid





PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
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PR 29-OCT-1999; 99US-0162142P.

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Db 1 AGAGAGACAATAATCAGTTTCGTGTGTTGGAGAGAAGAACAGATCAAATACGAG 60

QY 1234 GAGAGATCTCTAAGAGATTATCGTTTCAA 1264
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Db 61 GAGAGATCTCTAAGAGATTATCGTTTCAA 91

RESULT 5
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ID AAC37034 standard; DNA; 1001 BP.
XX
AC AAC37034;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15944.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
XX
PN EP1033405-A2.
PD
PE 06-SEP-2000.
PF
PF 25-FEB-2000; 2000EP-00301439.
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
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PR	04-OCT-1999;	99US-0157117P.										
PR	05-OCT-1999;	99US-0157753P.										
PR	06-OCT-1999;	99US-0157865P.										
PR	07-OCT-1999;	99US-0158029P.										
PR	08-OCT-1999;	99US-0158832P.										
PR	12-OCT-1999;	99US-0158869P.										
PR	13-OCT-1999;	99US-0159293P.										
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PR	14-OCT-1999;	99US-0159329P.										
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PR	14-OCT-1999;	99US-0159331P.										
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PR	21-OCT-1999;	99US-0160815P.										
PR	22-OCT-1999;	99US-0160980P.										
PR	22-OCT-1999;	99US-0160981P.										
PR	22-OCT-1999;	99US-0160989P.										
PR	25-OCT-1999;	99US-0161040P.										
PR	25-OCT-1999;	99US-0161405P.										
PR	26-OCT-1999;	99US-0161406P.										
PR	26-OCT-1999;	99US-0161359P.										
PR	26-OCT-1999;	99US-0161360P.										
PR	26-OCT-1999;	99US-0161361P.										
PR	28-OCT-1999;	99US-0161920P.										
PR	28-OCT-1999;	99US-0161922P.										
PR	28-OCT-1999;	99US-0161993P.										
PR	29-OCT-1999;	99US-0162142P.										

Matches	91;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0
Qy	1174	AGAGAGACAAATTAATCACTTCGTTGCTGTTTCGAGAGAGAGAAACAGATCAATACGAG	1233						
Db	1	AGAGAGACAAATTAATCACTTCGTTGCTGTTTCGAGAGAGAGAAACAGATCAATACGAG	60						
Qy	1234	GAGAGATCTCTAAACAGAGATTTATCGTTTCAA	1264						
Db	61	GAGAGATCTCTAAAGAGATTTATCGTTTCAA	91						
RESULT 6									
AAC38110									
ID	AAC38110 standard; DNA; 495 BP.								
XX	AAC38110;								
AC	AAC38110;								
XX	17-OCT-2000 (first entry)								
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 19822.								
DE	Arabidopsis thaliana								
XX	Hybridisation assay; genetic mapping; gene expression control;								
KW	protein identification; signal transduction pathway; metabolic pathway;								
KW	promoter; termination sequence; ss.								
OS	Arabidopsis thaliana.								
XX	Arabidopsis thaliana.								
XX	EP1033405-A2.								
PD	06-SEP-2000.								
XX	25-FEB-2000; 2000EP-00301439.								
XX	25-FEB-1999; 99US-0121825P.								
PR	05-MAR-1999; 99US-0123180P.								
PR	09-MAR-1999; 99US-0123548P.								
PR	23-MAR-1999; 99US-0125788P.								
PR	25-MAR-1999; 99US-0126264P.								
PR	29-MAR-1999; 99US-0126785P.								
PR	01-APR-1999; 99US-0127462P.								
PR	06-APR-1999; 99US-0128234P.								
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PR	19-APR-1999; 99US-0130077P.								
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PR	23-APR-1999; 99US-0130510P.								
PR	23-APR-1999; 99US-0130891P.								
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PR	11-MAY-1999; 99US-0132863P.								
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PR	14-MAY-1999; 99US-0134219P.								
PR	14-MAY-1999; 99US-0134370P.								
PR	18-MAY-1999; 99US-0134768P.								
PR	19-MAY-1999; 99US-0134941P.								
PR	20-MAY-1999; 99US-0135124P.								
PR	21-MAY-1999; 99US-0135353P.								
PR	24-MAY-1999; 99US-0135629P.								
PR	25-MAY-1999; 99US-0136021P.								
PR	27-MAY-1999; 99US-0136392P.								
PR	28-MAY-1999; 99US-0136782P.								
PR	01-JUN-1999; 99US-0137222P.								
PR	03-JUN-1999; 99US-0137528P.								
PR	04-JUN-1999; 99US-0137502P.								
PR	07-JUN-1999; 99US-0137724P.								
PR	08-JUN-1999; 99US-0138094P.								

PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 28-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 08-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144332P.  
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PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.

PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151068P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 4.4%; Score 89; DB 3; Length 495;  
Best Local Similarity 100.0%; Pred. No. 3.7e-29;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1176 AGAGACAATTAATCAGTTTCGTGTGTTGGAGAGAGAGACAGATCAATACGAGGA 1235







CC manipulation of cells, particularly plant cells. (I) is also useful in  
 CC screening assays of various plant strains to determine the strains that  
 CC are best capable of withstanding a particular disease or environmental  
 CC stress. (II) and (III) are useful for screening of biologically active  
 CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical  
 CC pathways. The screened agents are useful in improved methods of treating  
 CC crops to prevent or treat disease. (II) are also useful in screening  
 CC programs to identify agents that mimic or enhance the action of tolerance  
 CC factors. Such agents are useful in improved methods of treating crops to  
 CC enhance their tolerance to environmental stress. (I) is also useful for  
 CC enhancing or inhibiting production of a biosynthetic product in a plant.  
 CC (III) is useful for identifying other mediators that may induce  
 CC expression of proteins of interest, for establishing the extent to which  
 CC any specific insect and/or pathogen is responsible for damage to a  
 CC particular plant, for identifying other mediators that enhance or induce  
 CC tolerance to environmental stress, for identifying factors involved in  
 CC biosynthetic pathways of nutritional, commercial, or medicinal value and  
 CC for identifying productions of nutritional, commercial or medicinal  
 CC value. (IV) is useful in the study of genetic function and regulation,  
 CC for alteration of the cellular metabolism and for screening compounds  
 CC that may affect the biological function of the gene or gene products.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from USPTO  
 CC at seqdata.uspto.gov/sequence.html?DocID=999909770445

XX Sequence 1088 BP; 270 A; 264 C; 179 G; 375 T; 0 U; 0 Other;

Query Match 2.6%; Score 53; DB 6; Length 1088;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-13;  
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1212 AGAAGAACAGATCAAAATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAA 1264  
 |||||||  
 DB 1066 AGAAGAACAGATCAAAATACGAGAGAGATCTCTAAAGAGATTATCGTTTCAA 1014

# RESULT 9

ADM03675/c  
 ID ADM03675 standard; cDNA; 2550 BP.

XX ADM03675;

XX 20-MAY-2004 (first entry)

XX Human cDNA of the invention SEQ ID NO:2360.

XX ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.

XX Homo sapiens.

XX EP1347046-A1.

XX 24-SEP-2003.

XX 12-APR-2002; 2002EP-00008400.

XX 22-MAR-2002; 2002JP-00137785.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Isono Y, Hito Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX WPI; 2003-723558/69.

DR P-PSDB; ADM06118.

XX New polynucleotides and polypeptides are useful in gene therapy, for  
 PT developing a diagnostic marker or medicines for regulating their  
 PT expression and activity, or as a target of gene therapy.

XX Claim 1; SEQ ID NO 2360; 305pp; English.

CC The invention relates to a novel human polynucleotide and the encoded  
 CC polypeptide. A polynucleotide of the invention may have a use in gene  
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful  
 CC as a primer for synthesizing the polynucleotide or as a probe for  
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are  
 CC useful in gene therapy, for developing a diagnostic marker or medicines  
 CC for regulating their expression and activity, or as a target of gene  
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides  
 CC are useful as pharmaceutical agents. The present sequence represents a  
 CC cDNA sequence of the invention.

XX Sequence 2550 BP; 729 A; 546 C; 616 G; 659 T; 0 U; 0 Other;

Query Match 1.1%; Score 23; DB 11; Length 2550;  
 Best Local Similarity 100.0%; Pred. No. 8.4;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1928 TATATTCTTTTGTGAAAAATAA 1950

DB 1783 TATATTCTTTTGTGAAAAATAA 1761

## RESULT 10

ABL98998

ID ABL98998 standard; cDNA; 427 BP.

XX ABL98998;

XX 25-JUN-2002 (first entry)

XX Mouse neuronal regeneration related polynucleotide SEQ ID NO 42.

XX Mouse; neuronal; regeneration; nerve cell; synaptic efficiency; memory;  
 KW learning disorder; serial analysis of gene expression; SAGE;  
 KW gene expression; hippocampus; ss.

XX Mus sp.

XX DE10048893-A1.

XX 11-APR-2002.

XX 02-OCT-2000; 2000DE-01048893.

XX 02-OCT-2000; 2000DE-01048893.

XX (LION-) LION BIOSCIENCE AG.

XX WPI; 2002-341428/38.

XX New nucleic acids involved in neuronal regeneration, useful in screening  
 PT for modulators of regeneration or synaptic efficiency, and potential  
 PT therapeutic agents.

XX Claim 5; Page 27; 38pp; German.

XX The invention relates to nucleic acids (ABL98957-ABL99004) involved in  
 CC regenerative neuronal processes and encoded proteins (ABB79405-ABB79409)  
 CC used to screen for compounds and potential therapeutic agents that  
 CC modulate nerve cell regeneration and/or synaptic efficiency. They may  
 CC also be used for treatment or diagnosis of defective or pathological  
 CC memory and learning conditions

XX Sequence 427 BP; 116 A; 85 C; 96 G; 130 T; 0 U; 0 Other;

Query Match 1.1%; Score 22; DB 6; Length 427;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1590 AAAAAAAATTTGAAAAAAA 1611

DB 8 AAAAAAAATTTGAAAAAAA 29

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RESULT 11
ABL98999/c
ID ABL98999 standard; cDNA; 427 BP.
XX
XX ABL98999;
AC
XX
XX
DT 25-JUN-2002 (first entry)
XX
DE Mouse neuronal regeneration related polynucleotide SEQ ID NO 43.
XX
XX Mouse; neuronal; regeneration; nerve cell; synaptic efficiency; memory;
KW learning disorder; serial analysis of gene expression; SAGE;
XX gene expression; hippocampus; ss.
XX
XX Mus sp.
OS
XX
XX DE10048893-A1.
PN
XX
XX 11-APR-2002.
PD
XX
XX 02-OCT-2000; 2000DE-01048893.
PF
XX
XX 02-OCT-2000; 2000DE-01048893.
PR
XX
XX (LION-) LION BIOSCIENCE AG.
PA
XX
XX WPI; 2002-341428/38.
DR
XX
XX New nucleic acids involved in neuronal regeneration, useful in screening
PT for modulators of regeneration or synaptic efficiency, and potential
PT therapeutic agents.
XX
XX Claim 5; Page 27; 38pp; German.
PS
XX
XX The invention relates to nucleic acids (ABL98957-ABL99004) involved in
CC regenerative neuronal processes and encoded proteins (ABB79405-ABB79409)
CC used to screen for compounds and potential therapeutic agents that
CC modulate nerve cell regeneration and/or synaptic efficiency. They may
CC also be used for treatment or diagnosis of defective or pathological
CC memory and learning conditions
XX
XX Sequence 427 BP; 130 A; 96 C; 85 G; 116 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 22; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1590 AAAAAAAAAATTTGAAAAAAAAA 1611
Db 420 AAAAAAAAAATTTGAAAAAAAAA 399
RESULT 12
AAI92210
ID AAI92210 standard; cDNA; 432 BP.
XX
XX AC
AC
XX
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 12270.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200164835-A2.
PN
XX
XX 07-SEP-2001.
PD
```

```
XX
XX 26-FEB-2001; 2001WO-US004927.
XX
XX 28-FEB-2000; 2000US-00515126.
PR
XX 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Tang YT, Liu C, Drmanac RT;
PI
XX WPI; 2001-514838/56.
XX
XX P-PSDB; AAO12279.
DR
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 1; SEQ ID NO 12270; 1399pp + Sequence Listing; English.
PS
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 432 BP; 144 A; 86 C; 87 G; 115 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 22; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 GGAAGAAAAAATAATTTTGTG 103
Db 323 GGAAGAAAAAATAATTTTGTG 344
RESULT 13
ABV60815/c
ID ABV60815 standard; cDNA; 468 BP.
XX
XX AC
AC
XX
XX 13-SEP-2002 (first entry)
DT
XX
DE Human prostate expression marker cDNA 60806.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200160860-A2.
PN
XX
XX 23-AUG-2001.
PD
XX
XX 20-FEB-2001; 2001WO-US005171.
PP
XX
XX 17-FEB-2000; 2000US-0183319P.
XX
XX 16-MAR-2000; 2000US-0189862P.
PR
XX 25-MAY-2000; 2000US-0207454P.
PR
XX 09-JUN-2000; 2000US-0211314P.
PR
XX 18-JUL-2000; 2000US-0219007P.
PR
XX 13-DEC-2000; 2000US-0255281P.
PR
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
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PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 11567; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 468 BP; 131 A; 114 C; 114 G; 109 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 22; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1590 AAAAAAAAAATTGAAAAAAAAA 1611
DB 149 AAAAAAAAAATTGAAAAAAAAA 128
RESULT 14
ID ADS51475 standard; cDNA; 2115 BP.
XX ADS51475;
XX
XX 02-DEC-2004 (first entry)
DT
DE Bacterial polynucleotide #6218.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.
XX
XX Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT
```

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PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 29905; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plants with
CC the recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 2115 BP; 738 A; 339 C; 336 G; 702 T; 0 U; 0 Other;
SQ
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Best Local Similarity 100.0%; Pred. No. 24;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1589 CAAAAAAAAATTGAAAAAAAAA 1610
DB 53 CAAAAAAAAATTGAAAAAAAAA 32
RESULT 15
AAV52213/c
ID AAV52213 standard; DNA; 9607 BP.
XX
XX AAV52213;
XX
XX 23-OCT-1998 (first entry)
DT
DE Streptococcus pneumoniae genome fragment SEQ ID NO:80.
XX
XX Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
KW computer readable medium; vaccine; pharmaceutical composition; ds.
XX
XX Streptococcus pneumoniae.
XX
XX WO9818931-A2.
XX
XX 07-MAY-1998.
XX
XX 30-OCT-1997; 97WO-US019588.
XX
XX 31-OCT-1996; 96US-0029960P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Kunsch CA, Choi GH, Dillon PJ, Rosen CA, Barash SC, Fannon M;
PI Dougherty BA;
XX
XX WPI; 1998-272225/24.
XX
XX Computer-readable medium with recorded Streptococcus pneumoniae
PT polynucleotide sequences - useful in diagnostic kits and assays, and
```

PT pharmaceutical compositions and vaccines for Streptococcus pneumoniae.  
XX  
PS Claim 1; Page 637-642; 1409pp; English.  
XX  
CC The present invention describes a computer readable medium which has the  
CC nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded  
CC on it, or a representative fragment or a sequence at least 95% identical  
CC to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1  
CC to 391 (AAV52134 to AAV52524) are genomic fragments from Streptococcus  
CC pneumoniae. The present invention also describes an isolated nucleic acid  
CC molecule encoding a homologue of any of the fragments of the S.pneumoniae  
CC genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced  
CC by a process comprising: (a) screening a genomic DNA library using as a  
CC probe a target sequence defined by any of the sequences in SEQ ID NO:1 to  
CC 391, identifying members of the library which contain sequences that  
CC hybridize to the target sequence and isolating the nucleic acid molecules  
CC from the members; or (b) isolating mRNA, DNA or cDNA produced from an  
CC organism, amplifying nucleic acid molecules whose nucleotide sequence is  
CC homologous to amplification primers derived from the fragment of the S.  
CC pneumoniae genome to prime the amplification and isolating the amplified  
CC sequences. The computer readable medium can be used in a computer-based  
CC system for identifying fragments of the S. pneumoniae genome of  
CC commercial importance, or expression modulating fragments of the S.  
CC pneumoniae genome. Products from the present invention can be used in  
CC diagnosis kits and assays, and pharmaceutical compositions and vaccines  
CC for S. pneumoniae  
XX  
SQ Sequence 9607 BP; 2789 A; 1852 C; 2311 G; 2655 T; 0 U; 0 Other;

Query Match 1.1%; Score 22; DB 2; Length 9607;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 32 TTCTCTTTCTATTATT 53  
Db 8125 TTCTCTTTCTATTATT 8104

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OM nucleic.- nucleic search, using sw model

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Title: US-10-643-676-1

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Searched: 1202784 seqs, 818138359 residues

Word size : 0

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Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 1	22	1.1	9607	3 US-08-961-527-80	Sequence 80, Appl
C 2	21	1.0	2267	3 US-09-142-569-5	Sequence 5, Appl
C 3	21	1.0	2267	4 US-09-495-448A-5	Sequence 5, Appl
C 4	21	1.0	2338	4 US-09-582-337-1	Sequence 1, Appl
C 5	21	1.0	2350	3 US-09-187-478-1	Sequence 1, Appl
C 6	21	1.0	2350	3 US-09-292-036-1	Sequence 1, Appl
C 7	21	1.0	40742	4 US-09-949-016-11751	Sequence 11751, A
C 8	21	1.0	40747	4 US-09-949-016-13097	Sequence 13097, A
C 9	20	1.0	20	4 US-09-823-634A-13	Sequence 13, Appl
C 10	20	1.0	20	4 US-09-823-647B-13	Sequence 13, Appl
C 11	20	1.0	240	4 US-09-248-796A-8498	Sequence 8498, Ap
C 12	20	1.0	381	4 US-09-601-198-173	Sequence 173, App
C 13	20	1.0	425	4 US-09-786-454A-1	Sequence 1, Appl
C 14	20	1.0	601	4 US-09-949-016-28079	Sequence 28079, A
C 15	20	1.0	601	4 US-09-949-016-42035	Sequence 42035, A
C 16	20	1.0	601	4 US-09-949-016-42036	Sequence 42036, A
C 17	20	1.0	601	4 US-09-949-016-162196	Sequence 162196, A
C 18	20	1.0	1094	3 US-09-173-514-5	Sequence 5, Appl
C 19	20	1.0	52874	4 US-09-949-016-14868	Sequence 14868, A
C 20	20	1.0	56131	4 US-09-949-016-12944	Sequence 12944, A
C 21	20	1.0	64291	4 US-09-949-016-16278	Sequence 16278, A
C 22	20	1.0	86947	4 US-09-949-016-11930	Sequence 11930, A
C 23	20	1.0	117410	4 US-09-949-016-12282	Sequence 12282, A
C 24	20	1.0	149971	4 US-09-949-016-13590	Sequence 13590, A
C 25	20	1.0	450395	4 US-09-949-016-15473	Sequence 15473, A
C 26	19	0.9	140	4 US-09-513-999C-33553	Sequence 33553, A
C 27	19	0.9	303	4 US-09-248-796A-10927	Sequence 10927, A

C 28	19	0.9	501	3 US-09-134-001C-2580	Sequence 2580, Ap
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C 41	19	0.9	601	4 US-09-949-016-137476	Sequence 137476, A
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C 52	19	0.9	1821	3 US-09-528-784A-6	Sequence 6, Appl
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C 85	19	0.9	69687	4 US-09-949-016-12890	Sequence 12890, A
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c 104	19	0.9	246240	2	US-08-724-394A-20	Sequence 20, Appl	177	18	0.9	601	4	US-09-949-016-180103	Sequence 180103, A
c 105	19	0.9	246240	2	US-08-724-394A-21	Sequence 21, Appl	178	18	0.9	601	4	US-09-949-016-180104	Sequence 180104, A
c 106	19	0.9	246240	2	US-08-724-394A-22	Sequence 22, Appl	179	18	0.9	601	4	US-09-949-016-185543	Sequence 185543, A
c 107	19	0.9	256171	4	US-09-949-016-12822	Sequence 12822, A	c 180	18	0.9	601	4	US-09-949-016-186115	Sequence 186115, A
c 108	19	0.9	256176	4	US-09-949-016-15524	Sequence 15524, A	181	18	0.9	606	3	US-09-385-982-60	Sequence 60, Appl
c 109	19	0.9	275110	4	US-09-949-016-12706	Sequence 12706, A	182	18	0.9	650	3	US-08-943-731-61	Sequence 61, Appl
c 110	19	0.9	275110	4	US-09-949-016-16070	Sequence 16070, A	c 183	18	0.9	722	3	US-08-998-416-780	Sequence 1011, Ap
c 111	19	0.9	580073	4	US-08-545-528D-1	Sequence 1, Appl	c 184	18	0.9	727	3	US-08-998-416-1011	Sequence 1011, Ap
c 112	19	0.9	784019	4	US-09-949-016-14033	Sequence 14033, A	c 185	18	0.9	882	3	US-09-134-001C-966	Sequence 966, App
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c 114	19	0.9	828152	4	US-09-949-016-12777	Sequence 12777, A	c 187	18	0.9	1026	4	US-09-248-796A-12786	Sequence 12786, A
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c 127	18	0.9	369	4	US-09-513-999C-25019	Sequence 25019, A	c 200	18	0.9	1761	3	US-09-404-879A-387	Sequence 387, App
c 128	18	0.9	438	4	US-09-248-796A-7056	Sequence 7056, Ap	c 201	18	0.9	1761	4	US-09-667-857-387	Sequence 387, App
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c 131	18	0.9	530	4	US-09-270-767-22311	Sequence 22311, A	c 204	18	0.9	1958	4	US-09-270-767-10697	Sequence 10697, A
c 132	18	0.9	544	4	US-09-270-767-9220	Sequence 9220, Ap	c 205	18	0.9	1981	4	US-09-720-317A-3	Sequence 3, Appl
c 133	18	0.9	544	4	US-09-270-767-24502	Sequence 24502, A	c 206	18	0.9	2017	1	US-07-667-276A-3	Sequence 3, Appl
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c 135	18	0.9	560	4	US-09-949-016-105698	Sequence 105698, A	c 208	18	0.9	2090	4	US-09-023-655-226	Sequence 226, App
c 136	18	0.9	601	4	US-09-949-016-30010	Sequence 30010, A	c 209	18	0.9	2136	4	US-09-134-000C-2065	Sequence 2065, Ap
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c 139	18	0.9	601	4	US-09-949-016-41719	Sequence 41719, A	c 212	18	0.9	2608	4	US-09-667-857-386	Sequence 386, App
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c 141	18	0.9	601	4	US-09-949-016-42565	Sequence 42565, A	c 214	18	0.9	2943	3	US-09-404-879A-385	Sequence 385, App
c 142	18	0.9	601	4	US-09-949-016-45542	Sequence 45542, A	c 215	18	0.9	2943	4	US-09-667-857-385	Sequence 385, App
c 143	18	0.9	601	4	US-09-949-016-47839	Sequence 47839, A	c 216	18	0.9	2996	3	US-09-404-879A-311	Sequence 311, App
c 144	18	0.9	601	4	US-09-949-016-52554	Sequence 52554, A	c 217	18	0.9	2996	4	US-09-338-933-311	Sequence 311, App
c 145	18	0.9	601	4	US-09-949-016-54997	Sequence 54997, A	c 218	18	0.9	2996	4	US-09-667-857-311	Sequence 311, App
c 146	18	0.9	601	4	US-09-949-016-63260	Sequence 63260, A	c 219	18	0.9	3015	4	US-09-710-279-3401	Sequence 3401, Ap
c 147	18	0.9	601	4	US-09-949-016-63261	Sequence 63261, A	c 220	18	0.9	3110	3	US-08-936-165A-257	Sequence 257, App
c 148	18	0.9	601	4	US-09-949-016-82593	Sequence 82593, A	c 221	18	0.9	3222	4	US-08-714-741-39	Sequence 39, Appl
c 149	18	0.9	601	4	US-09-949-016-88051	Sequence 88051, A	c 222	18	0.9	3291	1	US-08-021-601-1	Sequence 1, Appl
c 150	18	0.9	601	4	US-09-949-016-88052	Sequence 88052, A	c 223	18	0.9	3291	1	US-08-082-8498-1	Sequence 1, Appl
c 151	18	0.9	601	4	US-09-949-016-88053	Sequence 88053, A	c 224	18	0.9	3291	5	PCT-US94-01624-1	Sequence 1, Appl
c 152	18	0.9	601	4	US-09-949-016-88054	Sequence 88054, A	c 225	18	0.9	3807	4	US-09-949-016-5238	Sequence 5238, Ap
c 153	18	0.9	601	4	US-09-949-016-88055	Sequence 88055, A	c 226	18	0.9	3835	4	US-09-710-279-3433	Sequence 3433, Ap
c 154	18	0.9	601	4	US-09-949-016-89154	Sequence 89154, A	c 227	18	0.9	3993	4	US-09-710-279-3985	Sequence 3985, Ap
c 155	18	0.9	601	4	US-09-949-016-89155	Sequence 89155, A	c 228	18	0.9	6676	4	US-09-949-016-16533	Sequence 16533, A
c 156	18	0.9	601	4	US-09-949-016-105699	Sequence 105699, A	c 229	18	0.9	8107	4	US-09-335-586-3	Sequence 3, Appl
c 157	18	0.9	601	4	US-09-949-016-105700	Sequence 105700, A	c 230	18	0.9	8612	4	US-09-949-016-16810	Sequence 16810, A
c 158	18	0.9	601	4	US-09-949-016-126378	Sequence 126378, A	c 231	18	0.9	10007	3	US-09-410-464-13	Sequence 13, Appl
c 159	18	0.9	601	4	US-09-949-016-126379	Sequence 126379, A	c 232	18	0.9	10470	4	US-08-956-171E-20	Sequence 20, Appl
c 160	18	0.9	601	4	US-09-949-016-128453	Sequence 128453, A	c 233	18	0.9	10470	4	US-08-781-986A-20	Sequence 20, Appl
c 161	18	0.9	601	4	US-09-949-016-131765	Sequence 131765, A	c 234	18	0.9	12366	4	US-09-949-016-14782	Sequence 14782, A
c 162	18	0.9	601	4	US-09-949-016-132236	Sequence 132236, A	c 235	18	0.9	12860	4	US-09-949-016-13082	Sequence 13082, A
c 163	18	0.9	601	4	US-09-949-016-132237	Sequence 132237, A	c 236	18	0.9	12861	4	US-09-949-016-12223	Sequence 12223, A
c 164	18	0.9	601	4	US-09-949-016-148692	Sequence 148692, A	c 237	18	0.9	12861	4	US-09-949-016-13426	Sequence 13426, A
c 165	18	0.9	601	4	US-09-949-016-150377	Sequence 150377, A	c 238	18	0.9	14273	3	US-08-961-527-40	Sequence 40, Appl
c 166	18	0.9	601	4	US-09-949-016-152609	Sequence 152609, A	c 239	18	0.9	16883	4	US-09-949-016-14694	Sequence 14694, A
c 167	18	0.9	601	4	US-09-949-016-152610	Sequence 152610, A	c 240	18	0.9	18591	4	US-09-949-016-14719	Sequence 14719, A
c 168	18	0.9	601	4	US-09-949-016-152611	Sequence 152611, A	c 241	18	0.9	20599	4	US-09-949-016-14717	Sequence 14717, A
c 169	18	0.9	601	4	US-09-949-016-152612	Sequence 152612, A	c 242	18	0.9	20599	4	US-09-949-016-14478	Sequence 14478, A
c 170	18	0.9	601	4	US-09-949-016-152613	Sequence 152613, A	c 243	18	0.9	23766	4	US-09-949-016-13569	Sequence 13569, A
c 171	18	0.9	601	4	US-09-949-016-152862	Sequence 152862, A	c 244	18	0.9	23781	4	US-09-949-016-13446	Sequence 13446, A
c 172	18	0.9	601	4	US-09-949-016-158992	Sequence 158992, A	c 245	18	0.9	24639	4	US-09-949-016-14068	Sequence 14068, A
c 173	18	0.9	601	4	US-09-949-016-160739	Sequence 160739, A	c 246	18	0.9	24715	4	US-09-949-016-12979	Sequence 12979, A



c 247	18	0.9	27491	4	US-09-949-016-12442	Sequence 12442, A	18	0.9	121068	4	US-09-949-016-14138	Sequence 14138, A
c 248	18	0.9	28283	4	US-09-949-016-15248	Sequence 15248, A	18	0.9	123513	4	US-09-949-016-15794	Sequence 15794, A
c 249	18	0.9	28393	4	US-09-949-016-16980	Sequence 16980, A	18	0.9	124480	4	US-09-949-016-15921	Sequence 15921, A
c 250	18	0.9	29671	4	US-09-949-016-12229	Sequence 12229, A	18	0.9	128175	4	US-09-949-016-16268	Sequence 16268, A
c 251	18	0.9	29671	4	US-09-949-016-17105	Sequence 17105, A	18	0.9	129899	4	US-09-949-016-16884	Sequence 16884, A
c 252	18	0.9	29717	4	US-09-949-016-16284	Sequence 16284, A	18	0.9	135667	4	US-09-949-016-15051	Sequence 15051, A
c 253	18	0.9	29769	4	US-09-949-016-16422	Sequence 16422, A	18	0.9	144158	4	US-09-949-016-11755	Sequence 11755, A
c 254	18	0.9	30324	4	US-09-949-016-16037	Sequence 16037, A	18	0.9	144158	4	US-09-949-016-12936	Sequence 12936, A
c 255	18	0.9	31000	4	US-09-966-451-10	Sequence 10, Appl	18	0.9	147321	4	US-09-949-016-15450	Sequence 15450, A
c 256	18	0.9	33109	4	US-09-949-016-14301	Sequence 14301, A	18	0.9	148156	4	US-09-949-016-11776	Sequence 11776, A
c 257	18	0.9	33870	4	US-09-949-016-16306	Sequence 16306, A	18	0.9	149371	4	US-09-949-016-13590	Sequence 13590, A
c 258	18	0.9	34855	4	US-09-949-016-13004	Sequence 13004, A	18	0.9	150597	4	US-09-949-016-13579	Sequence 13579, A
c 259	18	0.9	35285	4	US-09-949-016-13265	Sequence 13265, A	18	0.9	152231	3	US-09-128-155-16	Sequence 16, Appl
c 260	18	0.9	38326	4	US-09-949-016-15843	Sequence 15843, A	18	0.9	152486	4	US-09-949-016-12869	Sequence 12869, A
c 261	18	0.9	38582	3	US-08-943-731-2	Sequence 2, Appl	18	0.9	155019	4	US-09-949-016-16029	Sequence 16029, A
c 262	18	0.9	39755	4	US-09-949-016-17352	Sequence 17352, A	18	0.9	155617	4	US-09-949-016-16191	Sequence 16191, A
c 263	18	0.9	40219	4	US-09-949-016-15337	Sequence 15337, A	18	0.9	161124	4	US-09-949-016-11760	Sequence 11760, A
c 264	18	0.9	40315	4	US-09-949-016-11753	Sequence 11753, A	18	0.9	178883	4	US-09-949-016-12733	Sequence 12733, A
c 265	18	0.9	40649	4	US-09-949-016-14219	Sequence 14219, A	18	0.9	178884	4	US-09-949-016-13039	Sequence 13039, A
c 266	18	0.9	41100	4	US-09-755-665-46	Sequence 46, Appl	18	0.9	181251	4	US-09-949-016-15970	Sequence 15970, A
c 267	18	0.9	41639	4	US-09-949-016-15471	Sequence 15471, A	18	0.9	183770	4	US-09-949-016-15494	Sequence 15494, A
c 268	18	0.9	43576	4	US-09-676-519-19	Sequence 19, Appl	18	0.9	187595	4	US-09-949-016-15546	Sequence 15546, A
c 269	18	0.9	44244	4	US-09-949-016-11743	Sequence 11743, A	18	0.9	203475	4	US-09-949-016-14516	Sequence 14516, A
c 270	18	0.9	44245	4	US-09-949-016-13579	Sequence 13579, A	18	0.9	203475	4	US-09-949-016-14517	Sequence 14517, A
c 271	18	0.9	44342	4	US-09-949-016-12661	Sequence 12661, A	18	0.9	203475	4	US-09-949-016-14518	Sequence 14518, A
c 272	18	0.9	44821	4	US-09-949-016-13764	Sequence 13764, A	18	0.9	203475	4	US-09-949-016-14519	Sequence 14519, A
c 273	18	0.9	45183	4	US-09-949-016-12798	Sequence 12798, A	18	0.9	203475	4	US-09-949-016-17226	Sequence 17226, A
c 274	18	0.9	47419	4	US-09-949-016-11841	Sequence 11841, A	18	0.9	203475	4	US-09-949-016-17227	Sequence 17227, A
c 275	18	0.9	47420	4	US-09-949-016-15484	Sequence 15484, A	18	0.9	203475	4	US-09-949-016-17228	Sequence 17228, A
c 276	18	0.9	56302	4	US-09-949-016-11892	Sequence 11892, A	18	0.9	222452	4	US-09-949-016-12968	Sequence 12968, A
c 277	18	0.9	57392	4	US-09-949-016-12070	Sequence 12070, A	18	0.9	227979	4	US-09-949-016-11842	Sequence 11842, A
c 278	18	0.9	57402	4	US-09-949-016-13293	Sequence 13293, A	18	0.9	228896	4	US-09-949-016-17127	Sequence 17127, A
c 279	18	0.9	57875	4	US-09-949-016-13152	Sequence 13152, A	18	0.9	237510	4	US-09-949-016-14273	Sequence 14273, A
c 280	18	0.9	60376	4	US-09-949-016-12423	Sequence 12423, A	18	0.9	312474	4	US-09-949-016-17434	Sequence 17434, A
c 281	18	0.9	63563	4	US-09-596-002-33	Sequence 33, Appl	18	0.9	319608	4	US-09-539-333D-1	Sequence 1, Appl
c 282	18	0.9	64467	4	US-10-274-409-3	Sequence 3, Appl	18	0.9	319608	4	US-09-679-409-1	Sequence 1, Appl
c 283	18	0.9	64467	4	US-09-949-016-13968	Sequence 13968, A	18	0.9	390416	4	US-09-949-016-16923	Sequence 16923, A
c 284	18	0.9	68444	4	US-09-949-016-12361	Sequence 12361, A	18	0.9	636591	4	US-09-949-016-11808	Sequence 11808, A
c 285	18	0.9	69874	4	US-09-949-016-13049	Sequence 13049, A	18	0.9	636591	4	US-09-949-016-13388	Sequence 13388, A
c 286	18	0.9	72992	4	US-09-949-016-17592	Sequence 17592, A	18	0.9	640861	4	US-09-790-988-1	Sequence 1, Appl
c 287	18	0.9	72992	4	US-09-949-016-17592	Sequence 17592, A	18	0.9	670689	4	US-09-949-016-12505	Sequence 12505, A
c 288	18	0.9	72992	4	US-09-949-016-17592	Sequence 17592, A	18	0.9	670690	4	US-09-949-016-14207	Sequence 14207, A
c 289	18	0.9	76281	4	US-09-949-016-12708	Sequence 12708, A	18	0.9	767677	4	US-09-949-016-12147	Sequence 12147, A
c 290	18	0.9	80355	4	US-09-949-016-12735	Sequence 12735, A	18	0.9	767677	4	US-09-949-016-17361	Sequence 17361, A
c 291	18	0.9	80357	4	US-09-949-016-13572	Sequence 13572, A	18	0.9	1230025	4	US-09-198-452A-1	Sequence 1, Appl
c 292	18	0.9	81819	4	US-09-949-016-16661	Sequence 16661, A	18	0.9	1230025	4	US-09-438-185A-1	Sequence 1, Appl
c 293	18	0.9	81819	4	US-09-949-016-16662	Sequence 16662, A	18	0.9	1230230	4	US-08-916-421B-1	Sequence 1, Appl
c 294	18	0.9	84132	4	US-09-949-016-16562	Sequence 16562, A	18	0.9	1664976	4	US-08-916-421B-1	Sequence 1, Appl
c 295	18	0.9	85122	4	US-09-949-016-14693	Sequence 14693, A	18	0.9	1664976	4	US-09-692-570-1	Sequence 1, Appl
c 296	18	0.9	85963	4	US-09-949-016-13804	Sequence 13804, A	18	0.9	1664976	4	US-09-692-570-1	Sequence 1, Appl
c 297	18	0.9	87350	3	US-08-781-891-79	Sequence 79, Appl	17	0.8	17	4	US-09-866-108A-9901	Sequence 9901, Ap
c 298	18	0.9	87350	4	US-09-618-166-79	Sequence 79, Appl	17	0.8	17	4	US-09-866-108A-14793	Sequence 14793, A
c 299	18	0.9	87350	4	US-09-791-211-3	Sequence 3, Appl	17	0.8	25	4	US-09-866-108A-14794	Sequence 14794, A
c 300	18	0.9	87567	4	US-09-949-016-13335	Sequence 13335, A	17	0.8	25	4	US-09-866-108A-14795	Sequence 14795, A
c 301	18	0.9	88240	4	US-09-949-016-16279	Sequence 16279, A	17	0.8	25	4	US-09-866-108A-14796	Sequence 14796, A
c 302	18	0.9	90150	4	US-09-949-016-17383	Sequence 17383, A	17	0.8	25	4	US-09-866-108A-14797	Sequence 14797, A
c 303	18	0.9	92227	4	US-09-949-016-11929	Sequence 11929, A	17	0.8	25	4	US-09-866-108A-14798	Sequence 14798, A
c 304	18	0.9	92232	4	US-09-949-016-15421	Sequence 15421, A	17	0.8	25	4	US-09-866-108A-14799	Sequence 14799, A
c 305	18	0.9	93920	4	US-09-949-016-12461	Sequence 12461, A	17	0.8	25	4	US-09-866-108A-14800	Sequence 14800, A
c 306	18	0.9	93920	4	US-09-949-016-16853	Sequence 16853, A	17	0.8	25	4	US-09-866-108A-14801	Sequence 14801, A
c 307	18	0.9	95648	4	US-09-949-016-13139	Sequence 13139, A	17	0.8	25	4	US-09-866-108A-14802	Sequence 14802, A
c 308	18	0.9	96922	4	US-09-949-016-17061	Sequence 17061, A	17	0.8	25	4	US-09-866-108A-14803	Sequence 14803, A
c 309	18	0.9	100836	4	US-09-949-016-12871	Sequence 12871, A	17	0.8	25	4	US-09-866-108A-14804	Sequence 14804, A
c 310	18	0.9	100837	4	US-09-949-016-17063	Sequence 17063, A	17	0.8	25	4	US-09-866-108A-14805	Sequence 14805, A
c 311	18	0.9	100877	4	US-09-949-016-13276	Sequence 13276, A	17	0.8	25	4	US-09-866-108A-14806	Sequence 14806, A
c 312	18	0.9	100928	4	US-09-949-016-16926	Sequence 16926, A	17	0.8	25	4	US-09-866-108A-14807	Sequence 14807, A
c 313	18	0.9	101128	4	US-09-949-016-14293	Sequence 14293, A	17	0.8	25	4	US-09-866-108A-14808	Sequence 14808, A
c 314	18	0.9	103987	4	US-09-949-016-12513	Sequence 12513, A	17	0.8	25	4	US-09-866-108A-14809	Sequence 14809, A
c 315	18	0.9	103988	4	US-09-949-016-17050	Sequence 17050, A	17	0.8	25	4	US-09-866-108A-14810	Sequence 14810, A
c 316	18	0.9	106199	4	US-09-949-016-12393	Sequence 12393, A	17	0.8	25	4	US-09-866-108A-14811	Sequence 14811, A
c 317	18	0.9	107980	4	US-09-949-016-14370	Sequence 14370, A	17	0.8	25	4	US-09-866-108A-14812	Sequence 14812, A
c 318	18	0.9	112112	4	US-09-949-016-15639	Sequence 15639, A	17	0.8	25	4	US-09-866-108A-14813	Sequence 14813, A
c 319	18	0.9	119214	4	US-09-949-016-12507	Sequence 12507, A	17	0.8	25	4	US-09-866-108A-14814	Sequence 14814, A

C 393	17	0.8	183	4	US-09-248-796A-10444	Sequence 10444, A	C 465	17	0.8	368	4	US-09-270-767-6135	Sequence 6135, Ap
C 394	17	0.8	199	1	US-08-330-108-4	Sequence 4, Appl1	C 467	17	0.8	368	4	US-09-270-767-21417	Sequence 21417, A
C 395	17	0.8	199	5	PCT-US92-10087-4	Sequence 4, Appl1	C 469	17	0.8	369	4	US-09-248-796A-9541	Sequence 9541, Ap
C 396	17	0.8	204	4	US-09-248-796A-10679	Sequence 10679, A	C 469	17	0.8	371	4	US-09-621-976-16048	Sequence 16048, A
C 397	17	0.8	205	4	US-08-956-171E-2401	Sequence 2401, Ap	C 470	17	0.8	387	4	US-09-270-767-2955	Sequence 2955, Ap
C 398	17	0.8	205	4	US-08-781-986A-2401	Sequence 2401, Ap	C 471	17	0.8	387	4	US-09-270-767-18237	Sequence 18237, A
C 399	17	0.8	206	4	US-09-513-999C-19662	Sequence 19662, A	C 472	17	0.8	391	4	US-09-702-705-57	Sequence 57, Appl
C 400	17	0.8	207	4	US-09-248-796A-8940	Sequence 8940, Ap	C 473	17	0.8	391	4	US-09-736-457-57	Sequence 57, Appl
C 401	17	0.8	207	4	US-09-248-796A-11501	Sequence 11501, A	C 474	17	0.8	391	4	US-09-614-124B-57	Sequence 57, Appl
C 402	17	0.8	210	4	US-09-543-681A-326	Sequence 326, App	C 475	17	0.8	391	4	US-09-671-325-57	Sequence 57, Appl
C 403	17	0.8	216	4	US-09-770-767-8716	Sequence 8716, Ap	C 476	17	0.8	391	4	US-09-589-184-57	Sequence 57, Appl
C 404	17	0.8	216	4	US-09-270-767-23998	Sequence 23998, A	C 477	17	0.8	391	4	US-09-658-824-57	Sequence 2976, Ap
C 405	17	0.8	218	4	US-09-513-999C-17093	Sequence 17093, A	C 478	17	0.8	399	4	US-09-270-767-2976	Sequence 2976, Ap
C 406	17	0.8	261	4	US-09-248-796A-11472	Sequence 11472, A	C 479	17	0.8	399	4	US-09-270-767-18258	Sequence 18258, A
C 407	17	0.8	270	4	US-09-248-796A-7983	Sequence 7983, Ap	C 480	17	0.8	402	3	US-09-134-001C-1967	Sequence 1967, Ap
C 408	17	0.8	272	4	US-09-621-976-16007	Sequence 16007, A	C 481	17	0.8	408	4	US-09-248-796A-8101	Sequence 8101, Ap
C 409	17	0.8	276	4	US-09-543-681A-2091	Sequence 2091, Ap	C 482	17	0.8	441	4	US-09-621-976-9912	Sequence 9912, Ap
C 410	17	0.8	276	4	US-09-621-976-16034	Sequence 16034, A	C 483	17	0.8	441	4	US-09-248-796A-3289	Sequence 3289, Ap
C 411	17	0.8	278	4	US-09-313-294A-1578	Sequence 1578, Ap	C 484	17	0.8	447	4	US-09-270-767-15243	Sequence 15243, A
C 412	17	0.8	279	4	US-09-621-976-16037	Sequence 16037, A	C 485	17	0.8	453	4	US-09-270-767-9807	Sequence 9807, Ap
C 413	17	0.8	280	4	US-09-621-976-16046	Sequence 16046, A	C 486	17	0.8	453	4	US-09-270-767-25089	Sequence 25089, A
C 414	17	0.8	281	4	US-09-621-976-16011	Sequence 16011, A	C 487	17	0.8	462	4	US-09-270-767-4088	Sequence 4088, Ap
C 415	17	0.8	281	4	US-09-621-976-16034	Sequence 16034, A	C 488	17	0.8	462	4	US-09-270-767-19370	Sequence 19370, A
C 416	17	0.8	281	4	US-09-621-976-16054	Sequence 16054, A	C 489	17	0.8	468	4	US-09-248-796A-5960	Sequence 5960, Ap
C 417	17	0.8	281	4	US-09-621-976-16059	Sequence 16059, A	C 490	17	0.8	471	4	US-09-270-767-8988	Sequence 8988, Ap
C 418	17	0.8	282	4	US-09-621-976-16016	Sequence 16016, A	C 491	17	0.8	471	4	US-09-270-767-24270	Sequence 24270, A
C 419	17	0.8	282	4	US-09-621-976-16029	Sequence 16029, A	C 492	17	0.8	472	4	US-09-270-767-6143	Sequence 6143, Ap
C 420	17	0.8	282	4	US-09-248-796A-10119	Sequence 10119, A	C 493	17	0.8	472	4	US-09-270-767-21425	Sequence 21425, A
C 421	17	0.8	286	4	US-09-621-976-11456	Sequence 11456, A	C 494	17	0.8	485	4	US-09-621-976-12239	Sequence 12239, A
C 422	17	0.8	289	4	US-09-313-294A-6782	Sequence 6782, Ap	C 495	17	0.8	497	4	US-09-270-767-9590	Sequence 9590, Ap
C 423	17	0.8	292	4	US-09-621-976-16009	Sequence 16009, A	C 496	17	0.8	497	4	US-09-270-767-24872	Sequence 24872, A
C 424	17	0.8	296	4	US-09-621-976-16021	Sequence 16021, A	C 497	17	0.8	500	4	US-09-866-108A-15750	Sequence 15750, A
C 425	17	0.8	296	4	US-09-621-976-16049	Sequence 16049, A	C 498	17	0.8	504	4	US-09-248-796A-1009	Sequence 1009, Ap
C 426	17	0.8	297	4	US-09-621-976-16022	Sequence 16022, A	C 499	17	0.8	525	3	US-08-941-185-1	Sequence 1, Appl1
C 427	17	0.8	301	4	US-09-270-767-5573	Sequence 5573, Ap	C 500	17	0.8	525	3	US-09-872-047-1	Sequence 1, Appl1
C 428	17	0.8	301	4	US-09-270-767-20855	Sequence 20855, A	C 501	17	0.8	543	4	US-09-540-236-1096	Sequence 1096, Ap
C 429	17	0.8	302	4	US-09-621-976-16017	Sequence 16017, A	C 502	17	0.8	543	4	US-09-270-767-8781	Sequence 8781, Ap
C 430	17	0.8	303	4	US-09-328-352-3583	Sequence 3583, Ap	C 503	17	0.8	552	4	US-09-270-767-24063	Sequence 24063, A
C 431	17	0.8	304	4	US-09-621-976-13024	Sequence 13024, A	C 504	17	0.8	567	4	US-09-248-796A-4827	Sequence 4827, Ap
C 432	17	0.8	305	4	US-09-621-976-16020	Sequence 16020, A	C 505	17	0.8	581	3	US-09-020-956-103	Sequence 103, App
C 433	17	0.8	306	4	US-09-621-976-16014	Sequence 16014, A	C 506	17	0.8	581	3	US-09-030-607-103	Sequence 103, App
C 434	17	0.8	306	4	US-09-621-976-16035	Sequence 16035, A	C 507	17	0.8	581	3	US-09-439-313-103	Sequence 103, App
C 435	17	0.8	306	4	US-09-621-976-16057	Sequence 16057, A	C 508	17	0.8	581	3	US-09-352-616A-103	Sequence 103, App
C 436	17	0.8	307	4	US-09-621-976-16030	Sequence 16030, A	C 509	17	0.8	581	3	US-09-232-149A-103	Sequence 103, App
C 437	17	0.8	315	4	US-09-621-976-16028	Sequence 16028, A	C 510	17	0.8	581	4	US-09-159-812-103	Sequence 103, App
C 438	17	0.8	318	4	US-09-621-976-16040	Sequence 16040, A	C 511	17	0.8	581	4	US-09-636-215-103	Sequence 103, App
C 439	17	0.8	318	4	US-09-248-796A-9989	Sequence 9989, Ap	C 512	17	0.8	581	4	US-09-685-166A-103	Sequence 103, App
C 440	17	0.8	318	4	US-09-513-999C-35723	Sequence 35723, A	C 513	17	0.8	581	4	US-09-115-453-103	Sequence 103, App
C 441	17	0.8	319	4	US-09-621-976-16055	Sequence 16055, A	C 514	17	0.8	581	4	US-09-688-489-103	Sequence 103, App
C 442	17	0.8	320	4	US-09-621-976-16056	Sequence 16056, A	C 515	17	0.8	581	4	US-09-679-426-103	Sequence 103, App
C 443	17	0.8	321	4	US-09-248-796A-13652	Sequence 13652, A	C 516	17	0.8	581	4	US-09-759-143-103	Sequence 103, App
C 444	17	0.8	324	4	US-09-621-976-16027	Sequence 16027, A	C 517	17	0.8	581	4	US-09-651-236-103	Sequence 103, App
C 445	17	0.8	326	4	US-09-621-976-16024	Sequence 16024, A	C 518	17	0.8	583	3	US-09-030-607-203	Sequence 203, App
C 446	17	0.8	329	4	US-09-621-976-16012	Sequence 16012, A	C 519	17	0.8	583	3	US-09-439-313-203	Sequence 203, App
C 447	17	0.8	329	4	US-09-621-976-16052	Sequence 16052, A	C 520	17	0.8	583	3	US-09-352-616A-203	Sequence 203, App
C 448	17	0.8	332	4	US-09-621-976-16053	Sequence 16053, A	C 521	17	0.8	583	3	US-09-232-149A-203	Sequence 203, App
C 449	17	0.8	333	4	US-09-621-976-16032	Sequence 16032, A	C 522	17	0.8	583	4	US-09-159-812-203	Sequence 203, App
C 450	17	0.8	334	4	US-09-621-976-16032	Sequence 16032, A	C 523	17	0.8	583	4	US-09-636-215-203	Sequence 203, App
C 451	17	0.8	334	4	US-09-621-976-16045	Sequence 16045, A	C 524	17	0.8	583	4	US-09-685-166A-203	Sequence 203, App
C 452	17	0.8	335	4	US-09-621-976-16044	Sequence 16044, A	C 525	17	0.8	583	4	US-09-115-453-203	Sequence 203, App
C 453	17	0.8	336	4	US-09-621-976-16013	Sequence 16013, A	C 526	17	0.8	583	4	US-09-688-489-203	Sequence 203, App
C 454	17	0.8	336	4	US-09-248-796A-8946	Sequence 8946, Ap	C 527	17	0.8	583	4	US-09-679-426-203	Sequence 203, App
C 455	17	0.8	338	4	US-09-621-976-19232	Sequence 19232, A	C 528	17	0.8	583	4	US-09-759-143-203	Sequence 203, App
C 456	17	0.8	339	4	US-09-621-976-16015	Sequence 16015, A	C 529	17	0.8	583	4	US-09-651-236-203	Sequence 203, App
C 457	17	0.8	346	4	US-09-513-999C-26181	Sequence 26181, A	C 530	17	0.8	600	4	US-09-270-767-6676	Sequence 6676, Ap
C 458	17	0.8	347	4	US-09-621-976-16026	Sequence 16026, A	C 531	17	0.8	600	4	US-09-270-767-21958	Sequence 21958, A
C 459	17	0.8	355	4	US-09-621-976-8475	Sequence 8475, Ap	C 532	17	0.8	601	4	US-09-949-016-21343	Sequence 21343, A
C 460	17	0.8	355	4	US-09-621-976-8488	Sequence 8488, Ap	C 533	17	0.8	601	4	US-09-949-016-22574	Sequence 22574, A
C 461	17	0.8	357	4	US-09-621-976-16058	Sequence 16058, A	C 534	17	0.8	601	4	US-09-949-016-23771	Sequence 23771, A
C 462	17	0.8	359	4	US-09-621-976-16008	Sequence 16008, A	C 535	17	0.8	601	4	US-09-949-016-24951	Sequence 24951, A
C 463	17	0.8	359	4	US-09-621-976-16019	Sequence 16019, A	C 536	17	0.8	601	4	US-09-949-016-25316	Sequence 25316, A
C 464	17	0.8	362	4	US-09-621-976-16010	Sequence 16010, A	C 537	17	0.8	601	4	US-09-949-016-25317	Sequence 25317, A
C 465	17	0.8	365	4	US-09-621-976-16042	Sequence 16042, A	C 538	17	0.8	601	4	US-09-949-016-25318	Sequence 25318, A

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543	17	0.8	601	4	US-09-949-016-28277	Sequence 28277, A	C 616	17	0.8	601	4	US-09-949-016-88382	Sequence 88382, A
544	17	0.8	601	4	US-09-949-016-28287	Sequence 28287, A	C 617	17	0.8	601	4	US-09-949-016-88872	Sequence 88872, A
545	17	0.8	601	4	US-09-949-016-29827	Sequence 29827, A	C 618	17	0.8	601	4	US-09-949-016-88873	Sequence 88873, A
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547	17	0.8	601	4	US-09-949-016-31741	Sequence 31741, A	C 620	17	0.8	601	4	US-09-949-016-88875	Sequence 88875, A
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551	17	0.8	601	4	US-09-949-016-33332	Sequence 33332, A	C 624	17	0.8	601	4	US-09-949-016-91657	Sequence 91657, A
552	17	0.8	601	4	US-09-949-016-34516	Sequence 34516, A	C 625	17	0.8	601	4	US-09-949-016-91658	Sequence 91658, A
553	17	0.8	601	4	US-09-949-016-36446	Sequence 36446, A	C 626	17	0.8	601	4	US-09-949-016-92987	Sequence 92987, A
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559	17	0.8	601	4	US-09-949-016-36668	Sequence 36668, A	C 632	17	0.8	601	4	US-09-949-016-105769	Sequence 105769, A
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563	17	0.8	601	4	US-09-949-016-39493	Sequence 39493, A	C 636	17	0.8	601	4	US-09-949-016-108216	Sequence 108216, A
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587	17	0.8	601	4	US-09-949-016-69587	Sequence 69587, A	C 660	17	0.8	601	4	US-09-949-016-124276	Sequence 124276, A
588	17	0.8	601	4	US-09-949-016-70854	Sequence 70854, A	C 661	17	0.8	601	4	US-09-949-016-124277	Sequence 124277, A
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593	17	0.8	601	4	US-09-949-016-73430	Sequence 73430, A	C 666	17	0.8	601	4	US-09-949-016-126385	Sequence 126385, A
594	17	0.8	601	4	US-09-949-016-73535	Sequence 73535, A	C 667	17	0.8	601	4	US-09-949-016-126388	Sequence 126388, A
595	17	0.8	601	4	US-09-949-016-74335	Sequence 74335, A	C 668	17	0.8	601	4	US-09-949-016-126389	Sequence 126389, A
596	17	0.8	601	4	US-09-949-016-76583	Sequence 76583, A	C 669	17	0.8	601	4	US-09-949-016-126389	Sequence 126389, A
597	17	0.8	601	4	US-09-949-016-76992	Sequence 76992, A	C 670	17	0.8	601	4	US-09-949-016-128420	Sequence 128420, A
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607	17	0.8	601	4	US-09-949-016-80260	Sequence 80260, A	C 680	17	0.8	601	4	US-09-949-016-134685	Sequence 134685, A
608	17	0.8	601	4	US-09-949-016-82250	Sequence 82250, A	C 681	17	0.8	601	4	US-09-949-016-135684	Sequence 135684, A
609	17	0.8	601	4	US-09-949-016-82571	Sequence 82571, A	C 682	17	0.8	601	4	US-09-949-016-136377	Sequence 136377, A
610	17	0.8	601	4	US-09-949-016-82572	Sequence 82572, A	C 683	17	0.8	601	4	US-09-949-016-136378	Sequence 136378, A
611	17	0.8	601	4	US-09-949-016-82854	Sequence 82854, A	C 684	17	0.8	601	4	US-09-949-016-137820	Sequence 137820, A
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688	17	0.8	601	4	US-09-949-016-139402	Sequence 139402,	c 761	17	0.8	601	4	Sequence 186332,
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c 691	17	0.8	601	4	US-09-949-016-140157	Sequence 140157,	c 764	17	0.8	601	4	Sequence 189366,
c 692	17	0.8	601	4	US-09-949-016-141922	Sequence 141922,	c 765	17	0.8	601	4	Sequence 189368,
c 693	17	0.8	601	4	US-09-949-016-141923	Sequence 141923,	c 766	17	0.8	601	4	Sequence 191234,
c 694	17	0.8	601	4	US-09-949-016-143177	Sequence 143177,	c 767	17	0.8	601	4	Sequence 193978,
c 695	17	0.8	601	4	US-09-949-016-143178	Sequence 143178,	c 768	17	0.8	601	4	Sequence 194598,
c 696	17	0.8	601	4	US-09-949-016-143738	Sequence 143738,	c 769	17	0.8	601	4	Sequence 194599,
c 697	17	0.8	601	4	US-09-949-016-144367	Sequence 144367,	c 770	17	0.8	601	4	Sequence 194903,
698	17	0.8	601	4	US-09-949-016-144968	Sequence 144968,	c 771	17	0.8	601	4	Sequence 194976,
c 699	17	0.8	601	4	US-09-949-016-149453	Sequence 149453,	c 772	17	0.8	601	4	Sequence 194977,
c 700	17	0.8	601	4	US-09-949-016-149454	Sequence 149454,	c 773	17	0.8	601	4	Sequence 196879,
701	17	0.8	601	4	US-09-949-016-151634	Sequence 151634,	c 774	17	0.8	601	4	Sequence 196880,
c 702	17	0.8	601	4	US-09-949-016-152576	Sequence 152576,	c 775	17	0.8	601	4	Sequence 197896,
c 703	17	0.8	601	4	US-09-949-016-153001	Sequence 153001,	c 776	17	0.8	601	4	Sequence 198544,
c 704	17	0.8	601	4	US-09-949-016-153399	Sequence 153399,	c 777	17	0.8	601	4	Sequence 198545,
c 705	17	0.8	601	4	US-09-949-016-153401	Sequence 153401,	c 778	17	0.8	601	4	Sequence 199144,
c 706	17	0.8	601	4	US-09-949-016-153402	Sequence 153402,	c 779	17	0.8	601	4	Sequence 206692,
707	17	0.8	601	4	US-09-949-016-153824	Sequence 153824,	c 780	17	0.8	602	4	Sequence 72, Appl
c 708	17	0.8	601	4	US-09-949-016-154976	Sequence 154976,	c 781	17	0.8	614	4	Sequence 1318, Ap
c 709	17	0.8	601	4	US-09-949-016-155006	Sequence 155006,	c 782	17	0.8	618	4	Sequence 17128, Ap
c 710	17	0.8	601	4	US-09-949-016-156270	Sequence 156270,	c 783	17	0.8	618	4	Sequence 22410, A
c 711	17	0.8	601	4	US-09-949-016-157408	Sequence 157408,	c 784	17	0.8	635	4	Sequence 3442, Ap
c 712	17	0.8	601	4	US-09-949-016-157409	Sequence 157409,	c 785	17	0.8	635	4	Sequence 18724, A
c 713	17	0.8	601	4	US-09-949-016-157515	Sequence 157515,	c 786	17	0.8	667	4	Sequence 5146, Ap
c 714	17	0.8	601	4	US-09-949-016-157516	Sequence 157516,	c 787	17	0.8	667	4	Sequence 20428, A
c 715	17	0.8	601	4	US-09-949-016-158573	Sequence 158573,	c 788	17	0.8	691	4	Sequence 437, App
716	17	0.8	601	4	US-09-949-016-161273	Sequence 161273,	c 789	17	0.8	694	4	Sequence 6951, Ap
c 717	17	0.8	601	4	US-09-949-016-161952	Sequence 161952,	c 790	17	0.8	694	4	Sequence 22233, A
c 718	17	0.8	601	4	US-09-949-016-161953	Sequence 161953,	c 791	17	0.8	700	3	Sequence 302, App
c 719	17	0.8	601	4	US-09-949-016-162397	Sequence 162397,	c 792	17	0.8	703	4	Sequence 674, App
c 720	17	0.8	601	4	US-09-949-016-162992	Sequence 162992,	c 793	17	0.8	714	3	Sequence 863, App
c 721	17	0.8	601	4	US-09-949-016-163027	Sequence 163027,	c 794	17	0.8	714	3	Sequence 1139, Ap
c 722	17	0.8	601	4	US-09-949-016-163028	Sequence 163028,	c 795	17	0.8	722	3	Sequence 680, App
c 723	17	0.8	601	4	US-09-949-016-163120	Sequence 163120,	c 796	17	0.8	723	3	Sequence 1055, Ap
c 724	17	0.8	601	4	US-09-949-016-163137	Sequence 163137,	c 797	17	0.8	732	4	Sequence 1557, Ap
c 725	17	0.8	601	4	US-09-949-016-163138	Sequence 163138,	c 798	17	0.8	761	3	Sequence 382, App
c 726	17	0.8	601	4	US-09-949-016-163924	Sequence 163924,	c 799	17	0.8	771	4	Sequence 682, Ap
c 727	17	0.8	601	4	US-09-949-016-165310	Sequence 165310,	c 800	17	0.8	771	4	Sequence 2455, Ap
c 728	17	0.8	601	4	US-09-949-016-166280	Sequence 166280,	c 801	17	0.8	810	4	Sequence 29360, A
c 729	17	0.8	601	4	US-09-949-016-169126	Sequence 169126,	c 802	17	0.8	810	4	Sequence 10727, A
730	17	0.8	601	4	US-09-949-016-171844	Sequence 171844,	c 803	17	0.8	822	3	Sequence 8, Appli
c 731	17	0.8	601	4	US-09-949-016-171845	Sequence 171845,	c 804	17	0.8	822	3	Sequence 8, Appli
c 732	17	0.8	601	4	US-09-949-016-171847	Sequence 171847,	c 805	17	0.8	825	4	Sequence 6013, Ap
c 733	17	0.8	601	4	US-09-949-016-171848	Sequence 171848,	c 806	17	0.8	848	4	Sequence 14, Appl
c 734	17	0.8	601	4	US-09-949-016-172949	Sequence 172949,	c 807	17	0.8	886	4	Sequence 25354, A
c 735	17	0.8	601	4	US-09-949-016-173974	Sequence 173974,	c 808	17	0.8	917	4	Sequence 28085, A
c 736	17	0.8	601	4	US-09-949-016-173976	Sequence 173976,	c 809	17	0.8	918	4	Sequence 1982, Ap
c 737	17	0.8	601	4	US-09-949-016-173977	Sequence 173977,	c 810	17	0.8	927	4	Sequence 440, App
c 738	17	0.8	601	4	US-09-949-016-173978	Sequence 173978,	c 811	17	0.8	950	4	Sequence 8, Appli
c 739	17	0.8	601	4	US-09-949-016-174496	Sequence 174496,	c 812	17	0.8	950	4	Sequence 1507, Ap
c 740	17	0.8	601	4	US-09-949-016-175498	Sequence 175498,	c 813	17	0.8	1158	4	Sequence 2507, Ap
c 741	17	0.8	601	4	US-09-949-016-177418	Sequence 177418,	c 814	17	0.8	1167	4	Sequence 141, App
742	17	0.8	601	4	US-09-949-016-178223	Sequence 178223,	c 815	17	0.8	1196	4	Sequence 5074, Ap
c 743	17	0.8	601	4	US-09-949-016-178752	Sequence 178752,	c 816	17	0.8	1196	4	Sequence 20356, A
c 744	17	0.8	601	4	US-09-949-016-182541	Sequence 182541,	c 817	17	0.8	1205	4	Sequence 123, App
c 745	17	0.8	601	4	US-09-949-016-182542	Sequence 182542,	c 818	17	0.8	1220	2	Sequence 3, Appli
c 746	17	0.8	601	4	US-09-949-016-182552	Sequence 182552,	c 819	17	0.8	1220	3	Sequence 3, Appli
c 747	17	0.8	601	4	US-09-949-016-182661	Sequence 182661,	c 820	17	0.8	1220	3	Sequence 3, Appli
c 748	17	0.8	601	4	US-09-949-016-182662	Sequence 182662,	c 821	17	0.8	1220	3	Sequence 3, Appli
c 749	17	0.8	601	4	US-09-949-016-182672	Sequence 182672,	c 822	17	0.8	1246	4	Sequence 15706, A
c 750	17	0.8	601	4	US-09-949-016-183236	Sequence 183236,	c 823	17	0.8	1274	4	Sequence 72, Appl
c 751	17	0.8	601	4	US-09-949-016-183237	Sequence 183237,	c 824	17	0.8	1276	3	Sequence 2, Appli
c 752	17	0.8	601	4	US-09-949-016-183238	Sequence 183238,	c 825	17	0.8	1276	3	Sequence 2, Appli
c 753	17	0.8	601	4	US-09-949-016-183676	Sequence 183676,	c 826	17	0.8	1276	3	Sequence 2, Appli
c 754	17	0.8	601	4	US-09-949-016-183863	Sequence 183863,	c 827	17	0.8	1278	4	Sequence 1754, Ap
c 755	17	0.8	601	4	US-09-949-016-184739	Sequence 184739,	c 828	17	0.8	1287	4	Sequence 2170, Ap
c 756	17	0.8	601	4	US-09-949-016-185536	Sequence 185536,	c 829	17	0.8	1296	4	Sequence 1947, Ap
c 757	17	0.8	601	4	US-09-949-016-185623	Sequence 185623,	c 830	17	0.8	1305	6	Patent No. 5212087

C 831	17	0.8	1305	6	5212087-1	Patent No. 5212087	904	17	0.8	2412	1	US-08-437-027-18	Sequence 18, Appl
C 832	17	0.8	1370	4	US-09-663-600A-47	Sequence 47, Appl	905	17	0.8	2474	4	US-09-270-767-10028	Sequence 10028, A
C 833	17	0.8	1377	4	US-09-949-016-3717	Sequence 1717, Ap	C 906	17	0.8	2508	4	US-09-949-016-2289	Sequence 2289, Ap
C 834	17	0.8	1384	4	US-09-461-325-24	Sequence 24, Appl	907	17	0.8	2552	4	US-09-270-767-15247	Sequence 15247, A
C 835	17	0.8	1384	4	US-10-012-542-24	Sequence 24, Appl	908	17	0.8	2582	4	US-09-480-017-3	Sequence 3, Appl
C 836	17	0.8	1384	4	US-10-115-123-24	Sequence 24, Appl	909	17	0.8	2588	3	US-09-543-684A-1162	Sequence 1162, Ap
C 837	17	0.8	1398	4	US-09-710-279-1675	Sequence 1675, Ap	910	17	0.8	2754	4	US-09-248-796A-4857	Sequence 4857, Ap
C 838	17	0.8	1421	4	US-09-270-767-12333	Sequence 12333, A	911	17	0.8	2760	4	US-09-248-796A-1053	Sequence 1053, Ap
C 839	17	0.8	1422	4	US-09-248-796A-1981	Sequence 1981, Ap	C 912	17	0.8	2782	4	US-09-134-001C-2477	Sequence 4372, Ap
C 840	17	0.8	1426	4	US-09-620-312B-967	Sequence 967, App	913	17	0.8	2797	4	US-09-949-016-376	Sequence 376, App
C 841	17	0.8	1443	4	US-09-270-767-13193	Sequence 13193, A	914	17	0.8	2848	3	US-08-539-205A-3	Sequence 3, Appl
C 842	17	0.8	1455	3	US-09-134-001C-2226	Sequence 2226, Ap	C 915	17	0.8	2848	4	US-09-392-163A-3	Sequence 3, Appl
C 843	17	0.8	1457	4	US-09-638-937-1	Sequence 1, Appl	917	17	0.8	2862	4	US-09-499-203-13	Sequence 13, Appl
C 844	17	0.8	1457	4	US-09-949-016-2761	Sequence 2761, Ap	918	17	0.8	2893	4	US-09-270-767-26336	Sequence 26336, A
C 845	17	0.8	1484	4	US-08-956-171B-595	Sequence 595, App	919	17	0.8	2973	1	US-08-451-715A-7	Sequence 7, Appl
C 846	17	0.8	1484	4	US-08-781-986A-595	Sequence 595, App	920	17	0.8	2976	4	US-09-386-963C-7	Sequence 7, Appl
C 847	17	0.8	1499	4	US-09-023-655-80	Sequence 80, Appl	921	17	0.8	2976	4	US-09-386-959-7	Sequence 7, Appl
C 848	17	0.8	1500	3	US-09-593-711A-10	Sequence 10, Appl	922	17	0.8	2976	4	US-09-386-959-7	Sequence 7, Appl
C 849	17	0.8	1647	4	US-09-248-796A-406	Sequence 406, App	C 923	17	0.8	3001	4	US-09-539-333D-205	Sequence 205, App
C 850	17	0.8	1666	4	US-09-799-451-479	Sequence 479, App	924	17	0.8	3007	4	US-09-710-279-3846	Sequence 3846, Ap
C 851	17	0.8	1668	4	US-09-270-767-31595	Sequence 31595, A	925	17	0.8	3020	4	US-09-220-132-19	Sequence 19, Appl
C 852	17	0.8	1698	4	US-09-861-451A-31	Sequence 31, Appl	C 926	17	0.8	3090	4	US-09-710-279-3599	Sequence 3599, Ap
C 853	17	0.8	1700	1	US-08-539-304A-3	Sequence 3, Appl	927	17	0.8	3100	3	US-08-936-165A-184	Sequence 184, App
C 854	17	0.8	1710	3	US-09-134-001C-2735	Sequence 2735, Ap	C 928	17	0.8	3304	4	US-09-710-279-3740	Sequence 3740, Ap
C 855	17	0.8	1728	4	US-09-614-221A-461	Sequence 461, App	928	17	0.8	3467	3	US-09-298-924-3	Sequence 3, Appl
C 856	17	0.8	1728	4	US-09-149-476-277	Sequence 277, App	929	17	0.8	3467	4	US-09-743-492A-1	Sequence 1, Appl
C 857	17	0.8	1746	4	US-09-147-405B-12	Sequence 12, Appl	C 930	17	0.8	3477	4	US-09-513-505-10	Sequence 10, Appl
C 858	17	0.8	1747	4	US-08-956-171B-685	Sequence 685, App	931	17	0.8	3585	4	US-09-270-767-14479	Sequence 14, Appl
C 859	17	0.8	1747	4	US-08-781-986A-685	Sequence 685, App	C 932	17	0.8	3600	4	US-09-147-405B-14	Sequence 14, Appl
C 860	17	0.8	1760	1	US-08-413-118-117	Sequence 117, App	933	17	0.8	3600	5	PCT-US95-13749-1	Sequence 10858, A
C 861	17	0.8	1760	3	US-08-473-446-117	Sequence 117, Appl	934	17	0.8	3741	4	US-09-270-767-10858	Sequence 4214, A
C 862	17	0.8	1781	4	US-09-147-405B-10	Sequence 10, Appl	C 935	17	0.8	3816	4	US-09-710-279-4214	Sequence 28, Appl
C 863	17	0.8	1788	4	US-09-248-796A-459	Sequence 459, App	936	17	0.8	3898	5	US-08-471-791-28	Sequence 28, Appl
C 864	17	0.8	1821	4	US-09-205-258-43	Sequence 43, Appl	C 937	17	0.8	3938	2	PCT-US91-01746-28	Sequence 1, Appl
C 865	17	0.8	1830	2	US-08-933-750C-79	Sequence 79, Appl	938	17	0.8	3938	2	US-08-731-722-1	Sequence 1, Appl
C 866	17	0.8	1830	3	US-09-234-613-79	Sequence 79, Appl	C 939	17	0.8	3936	2	US-08-731-722-1	Sequence 2, Appl
C 867	17	0.8	1858	4	US-09-270-767-10460	Sequence 10460, A	940	17	0.8	3936	2	US-08-731-722-2	Sequence 2, Appl
C 868	17	0.8	1864	3	US-09-149-476-130	Sequence 130, App	C 941	17	0.8	3936	2	US-08-731-722-2	Sequence 3, Appl
C 869	17	0.8	1876	3	US-08-714-318-33	Sequence 33, Appl	942	17	0.8	3933	2	US-08-731-722-3	Sequence 3, Appl
C 870	17	0.8	1876	3	US-09-265-315-33	Sequence 33, Appl	C 943	17	0.8	3933	2	US-09-270-767-13399	Sequence 13399, A
C 871	17	0.8	1876	3	US-09-265-315-33	Sequence 33, Appl	944	17	0.8	4073	3	US-09-166-350-1	Sequence 1, Appl
C 872	17	0.8	1876	3	US-09-266-417-33	Sequence 33, Appl	C 945	17	0.8	4422	3	US-09-949-016-13991	Sequence 1, Appl
C 873	17	0.8	1876	4	US-09-528-709-33	Sequence 33, Appl	946	17	0.8	4422	3	US-09-949-016-13991	Sequence 5, Appl
C 874	17	0.8	1876	4	US-09-527-745-33	Sequence 33, Appl	947	17	0.8	4748	3	US-09-331-581-1	Sequence 5, Appl
C 875	17	0.8	1908	2	US-09-909-965C-17	Sequence 17, Appl	C 948	17	0.8	4916	4	US-09-866-108A-5	Sequence 14874, A
C 876	17	0.8	1919	4	US-09-949-016-220	Sequence 220, App	949	17	0.8	4982	4	US-09-949-016-14874	Sequence 241, App
C 877	17	0.8	1921	4	US-09-949-016-2094	Sequence 2094, Ap	C 950	17	0.8	5000	4	US-08-556-171E-241	Sequence 241, App
C 878	17	0.8	1931	4	US-09-976-594-329	Sequence 329, App	C 951	17	0.8	5000	4	US-08-781-986A-241	Sequence 241, App
C 879	17	0.8	1977	4	US-08-705-477E-99	Sequence 99, Appl	C 952	17	0.8	5075	4	US-09-949-016-100	Sequence 100, App
C 880	17	0.8	2056	4	US-09-498-557-20	Sequence 20, Appl	953	17	0.8	5089	6	5177197-31	Patent No. 5177197
C 881	17	0.8	2081	3	US-09-149-476-123	Sequence 123, App	954	17	0.8	5089	6	5177197-31	Patent No. 5177197
C 882	17	0.8	2099	4	US-09-949-016-2191	Sequence 2191, Ap	C 955	17	0.8	5310	4	US-09-620-312D-623	Sequence 623, App
C 883	17	0.8	2160	2	US-08-840-236-2	Sequence 2, Appl	956	17	0.8	5449	4	US-09-949-016-2138	Sequence 2138, Ap
C 884	17	0.8	2160	2	US-08-840-236-5	Sequence 5, Appl	C 957	17	0.8	5516	4	US-09-949-016-868	Sequence 868, App
C 885	17	0.8	2160	2	US-08-505-448A-2	Sequence 2, Appl	C 958	17	0.8	5605	3	US-09-268-140-6	Sequence 6, Appl
C 886	17	0.8	2160	2	US-08-505-448A-5	Sequence 5, Appl	C 959	17	0.8	5749	4	US-09-949-016-15441	Sequence 15441, A
C 887	17	0.8	2169	4	US-09-976-594-315	Sequence 315, App	C 960	17	0.8	5749	4	US-09-949-016-15442	Sequence 15442, A
C 888	17	0.8	2223	1	US-08-257-073-4	Sequence 4, Appl	C 961	17	0.8	5819	3	US-09-949-016-16028	Sequence 16028, A
C 889	17	0.8	2268	1	US-08-873-093-2	Sequence 2, Appl	962	17	0.8	5919	3	US-08-987-123-4	Sequence 4, Appl
C 890	17	0.8	2268	3	US-09-206-646-2	Sequence 2, Appl	C 963	17	0.8	6002	4	US-09-590-211A-18	Sequence 18, Appl
C 891	17	0.8	2280	1	US-08-220-151-11	Sequence 11, Appl	C 964	17	0.8	6027	4	US-09-620-312D-517	Sequence 517, App
C 892	17	0.8	2280	1	US-08-413-118-11	Sequence 11, Appl	965	17	0.8	6043	4	US-09-989-981A-9	Sequence 9, Appl
C 893	17	0.8	2280	4	US-08-473-446-11	Sequence 11, Appl	C 966	17	0.8	6055	4	US-09-953-318-10	Sequence 10, Appl
C 894	17	0.8	2287	4	US-09-561-763-7	Sequence 7, Appl	967	17	0.8	6204	3	US-09-499-203-20	Sequence 20, Appl
C 895	17	0.8	2287	4	US-09-431-367B-7	Sequence 7, Appl	C 968	17	0.8	6216	3	US-09-213-053-1	Sequence 1, Appl
C 896	17	0.8	2315	3	US-08-961-527-194	Sequence 194, App	C 969	17	0.8	6305	3	US-08-687-580B-6	Sequence 6, Appl
C 897	17	0.8	2331	4	US-09-866-028-54	Sequence 54, Appl	C 970	17	0.8	6356	4	US-09-770-595A-1	Sequence 1, Appl
C 898	17	0.8	2331	4	US-09-944-457-54	Sequence 54, Appl	C 971	17	0.8	6908	4	US-09-949-016-14842	Sequence 14842, A
C 899	17	0.8	2335	2	US-08-300-584-3	Sequence 3, Appl	972	17	0.8	7173	4	US-09-949-016-17491	Sequence 17491, A
C 900	17	0.8	2335	3	US-08-476-123-3	Sequence 3, Appl	973	17	0.8	7244	3	US-08-378-313-26	Sequence 26, Appl
C 901	17	0.8	2335	3	US-08-742-684A-3	Sequence 3, Appl	C 974	17	0.8	7286	3	US-09-331-581-3	Sequence 3, Appl
C 902	17	0.8	2368	4	US-09-270-767-9834	Sequence 9834, Ap	975	17	0.8	7387	4	US-09-499-203-17	Sequence 17, Appl
C 903	17	0.8	2409	3	US-09-484-970B-101	Sequence 101, App	C 976	17	0.8	7424	4	US-09-949-016-13898	Sequence 13898, A

977 17 0.8 7702 4 US-09-023-655-1336 Sequence 1336, Ap  
978 17 0.8 7702 4 US-09-743-492A-3 Sequence 3, Appli  
C 979 17 0.8 7707 4 US-09-866-108A-2 Sequence 2, Appli  
C 980 17 0.8 7716 4 US-09-949-016-16614 Sequence 16614, A  
981 17 0.8 7938 3 US-09-331-581-14 Sequence 14, Appli  
C 982 17 0.8 8117 4 US-09-866-108A-1 Sequence 1, Appli  
983 17 0.8 8205 4 US-09-949-016-1500 Sequence 1500, Ap  
984 17 0.8 8220 4 US-09-949-016-932 Sequence 932, App  
985 17 0.8 8405 4 US-09-949-016-11882 Sequence 11882, A  
986 17 0.8 8405 4 US-09-949-016-15376 Sequence 15376, A  
987 17 0.8 8641 4 US-09-949-016-14077 Sequence 14077, A  
C 988 17 0.8 8658 4 US-09-949-016-17038 Sequence 17038, A  
C 989 17 0.8 9098 4 US-09-358-082A-28 Sequence 28, Appli  
C 990 17 0.8 9098 4 US-09-358-082A-28 Sequence 28, Appli  
991 17 0.8 9169 4 US-09-949-016-11948 Sequence 11948, A  
992 17 0.8 9170 4 US-09-949-016-17079 Sequence 17079, A  
993 17 0.8 9321 4 US-09-499-203-1 Sequence 1, Appli  
C 994 17 0.8 9406 4 US-09-949-016-17494 Sequence 17494, A  
C 995 17 0.8 9527 4 US-09-949-016-13979 Sequence 13979, A  
996 17 0.8 9884 4 US-09-949-016-12548 Sequence 12548, A  
997 17 0.8 9889 4 US-09-949-016-16116 Sequence 16116, A  
C 998 17 0.8 10160 4 US-09-949-016-13215 Sequence 13215, A  
C 999 17 0.8 10207 1 US-08-920-812-2 Sequence 2, Appli  
C1000 17 0.8 10207 1 US-08-920-827-2 Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-08-961-527-80/c  
; Sequence 80, Application US/08961527  
; Patent No. 6420135  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 391  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,527  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P1  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 967 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-961-527-80  
Query Match 1.1%; Score 22; DB 3; Length 9607;  
Best Local Similarity 100.0%; Pred. No. 5.8;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 32 TTCTCTTTCTTTCTTTTATTT 53  
Db 8125 TTCTCTTTCTTTCTTTTATTT 8104  
RESULT 2  
US-09-142-569-5/c  
; Sequence 5, Application US/09142569  
; Patent No. 6413735  
; GENERAL INFORMATION:  
; APPLICANT: Lau, Lester F.  
; TITLE OF INVENTION: Extracellular Matrix Signalling Molecules  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/142,569  
; FILING DATE: 02-Apr-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W.  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28758/33766  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2267 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: "Figs12 cDNA coding sequence"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-142-569-5

Query Match 1.0%; Score 21; DB 3; Length 2267;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 199 TTTTCATATAAAATATATA 219  
Db 2256 TTTTCATATAAAATATATA 2236

RESULT 3  
US-09-495-448A-5/c  
; Sequence 5, Application US/09495448A  
; Patent No. 6790606  
; GENERAL INFORMATION:  
; APPLICANT: Lau, Lester F.  
; TITLE OF INVENTION: EXTRACELLULAR MATRIX SIGNALLING MOLECULES  
; FILE REFERENCE: 28758/36072 US/09/495,448A  
; CURRENT APPLICATION NUMBER: 2000-01-31  
; PRIOR APPLICATION NUMBER: 09/142,569  
; PRIOR FILING DATE: 1999-04-02

; PRIOR APPLICATION NUMBER: 60/013,958  
; PRIOR FILING DATE: 1996-03-15  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 2267  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; OTHER INFORMATION: Fisp12 cDNA coding sequence  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (138)..(1181)  
US-09-495-448A-5

Query Match 1.0%; Score 21; DB 4; Length 2267;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 TTTTCATATAAAATATATA 219  
|||||  
Db 2256 TTTTCATATAAAATATATA 2236

RESULT 4  
US-09-582-337-1/c  
; Sequence 1, Application US/09582337  
; Patent No. 6562618  
; GENERAL INFORMATION:  
; APPLICANT: Japan Tobacco, Inc.  
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor  
; FILE REFERENCE: JI-009PCI  
; CURRENT APPLICATION NUMBER: US/09/582,337  
; CURRENT FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: JP P1997-367699  
; PRIOR FILING DATE: 1997-12-25  
; PRIOR APPLICATION NUMBER: JP P1998-356183  
; PRIOR FILING DATE: 1998-12-15  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2338  
; TYPE: DNA  
; ORGANISM: Rat  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (1)..(212)  
; NAME/KEY: CDS  
; LOCATION: (213)..(1256)  
; NAME/KEY: 3'UTR  
; LOCATION: (1257)..(2338)  
; NAME/KEY: polyA signal  
; LOCATION: (2297)..(2302)  
US-09-582-337-1

Query Match 1.0%; Score 21; DB 4; Length 2338;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 TTTTCATATAAAATATATA 219  
|||||  
Db 2326 TTTTCATATAAAATATATA 2306

RESULT 5  
US-09-187-478-1/c  
; Sequence 1, Application US/09187478  
; Patent No. 6348329  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Brian F.  
; APPLICANT: Allen, Margaret L.  
; TITLE OF INVENTION: Connective Tissue Growth (CTGF) And Methods Of Use

; FILE REFERENCE: 08766/004001  
; CURRENT APPLICATION NUMBER: US/09/187,478  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2350  
; TYPE: DNA  
; ORGANISM: No. 6348329mal Rate Kidney Fibroblast  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (212)..(1252)  
US-09-187-478-1

Query Match 1.0%; Score 21; DB 3; Length 2350;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 TTTTCATATAAAATATATA 219  
|||||  
Db 2328 TTTTCATATAAAATATATA 2308

RESULT 6  
US-09-292-036-1/c  
; Sequence 1, Application US/09292036  
; Patent No. 6358741  
; GENERAL INFORMATION:  
; APPLICANT: FIBROGEN, INC  
; APPLICANT: SCHMIDT, Brian  
; APPLICANT: ALLEN, Margaret  
; APPLICANT: SVERDRUP, Fran  
; APPLICANT: CARMICHAEL, David  
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE  
; FILE REFERENCE: FIBRO100-1  
; CURRENT APPLICATION NUMBER: US/09/292,036  
; CURRENT FILING DATE: 1999-04-14  
; PRIOR APPLICATION NUMBER: US 09/292,036  
; PRIOR FILING DATE: 1999-04-14  
; PRIOR APPLICATION NUMBER: US 09/187,478  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 2350  
; TYPE: DNA  
; ORGANISM: Rat  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (212)..(1252)  
US-09-292-036-1

Query Match 1.0%; Score 21; DB 3; Length 2350;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 TTTTCATATAAAATATATA 219  
|||||  
Db 2328 TTTTCATATAAAATATATA 2308

RESULT 7  
US-09-949-016-11751/c  
; Sequence 11751, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755



```
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11751
; LENGTH: 40742
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11751

Query Match          1.0%; Score 21; DB 4; Length 40742;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      73 ATTACAAAAGGAAAAA 93
Db      38117 ATTACAAAAGGAAAAA 38097

RESULT 8
US-09-949-016-13097/c
; Sequence 13097, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13097
; LENGTH: 40747
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13097

Query Match          1.0%; Score 21; DB 4; Length 40747;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      73 ATTACAAAAGGAAAAA 93
Db      38117 ATTACAAAAGGAAAAA 38097

RESULT 9
US-09-823-634A-13
; Sequence 13, Application US/09823634A
; Patent No. 6596489
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Candida albicans
; NAME/KEY: unsure
; LOCATION: (156)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknown
US-09-823-634A-13
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-09-823-634A-13

Query Match          1.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1591 AAAAAAAATTTGAAAAA 1610
Db      1 AAAAAAAATTTGAAAAA 20

RESULT 10
US-09-823-647B-13
; Sequence 13, Application US/09823647B
; Patent No. 6596490
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-09-823-647B-13

Query Match          1.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1591 AAAAAAAATTTGAAAAA 1610
Db      1 AAAAAAAATTTGAAAAA 20

RESULT 11
US-09-248-796A-8498/c
; Sequence 8498, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 8498
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (156)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknown
US-09-248-796A-8498
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Query Match 1.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 AAAAGGAAAAAATAAT 97  
Db 138 AAAAGGAAAAAATAAT 119

## RESULT 12

US-09-601-198-173  
; Sequence 173, Application US/09601198  
; Patent No. 6531583  
; GENERAL INFORMATION:  
; APPLICANT: Cassell, Gail H.  
; APPLICANT: Chen, Ellison Y.  
; APPLICANT: Glass, Jennifer S.  
; APPLICANT: Glass, John I.  
; APPLICANT: Heiner, Cheryl R.  
; APPLICANT: Lefkowitz, Elliot  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA  
; FILE OF INVENTION: UREALYTICUM  
; FILE REFERENCE: UAB-13452/22  
; CURRENT APPLICATION NUMBER: US/09/601,198  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/073,189  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 181  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 173  
; LENGTH: 381  
; TYPE: DNA  
; ORGANISM: Ureaplasma urealyticum  
US-09-601-198-173

Query Match 1.0%; Score 20; DB 4; Length 381;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1969 GTTTATTAAATTGACAGATT 1988  
Db 138 GTTTATTAAATTGACAGATT 157

## RESULT 13

US-09-786-454A-1  
; Sequence 1, Application US/09786454A  
; Patent No. 6589532  
; GENERAL INFORMATION:  
; APPLICANT: De Villiers-Zur Hausen, Ethel-Michele  
; APPLICANT: Zur Hausen, Harald  
; TITLE OF INVENTION: PAPILLOMA VIRUSES, MEANS FOR THE DETECTION THEREOF AND THERAPY FOR  
; FILE OF INVENTION: DISEASES CAUSED THEREBY  
; FILE REFERENCE: 8484-097-999  
; CURRENT APPLICATION NUMBER: US/09/786,454A  
; CURRENT FILING DATE: 2001-07-31  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 425  
; TYPE: DNA  
; ORGANISM: Papillomavirus sylvilagi  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(423)  
US-09-786-454A-1

Query Match 1.0%; Score 20; DB 4; Length 425;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 880 AATTTTACTATTTGTACCGC 899  
|||||

Db 43 AATTTTACTATTTGTACCGC 62

## RESULT 14

US-09-949-016-28079  
; Sequence 28079, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 28079  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-28079

Query Match 1.0%; Score 20; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 TTTTCTATTTTATTGATT 57  
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Db 215 TTTTCTATTTTATTGATT 234

## RESULT 15

US-09-949-016-42035/c  
; Sequence 42035, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 42035  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-42035

Query Match 1.0%; Score 20; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 CATTACAAAAGGAAAAAAA 91  
|||||  
Db 372 CATTACAAAAGGAAAAAAA 353

Search completed: October 24, 2005, 06:43:30  
Job time : 905 secs

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81	20	1.0	423	12	US-09-925-065A-148530	Sequence 148530, A	c 154	20	1.0	4172	15	US-10-311-455-687	Sequence 687, App
82	20	1.0	423	12	US-09-925-065A-148533	Sequence 148533, A	c 155	20	1.0	4413	18	US-10-424-599-141147	Sequence 141147, A
83	20	1.0	423	12	US-09-925-065A-148534	Sequence 148534, A	c 156	20	1.0	5156	21	US-10-956-157-4159	Sequence 4159, App
C 84	20	1.0	439	12	US-09-925-065A-217402	Sequence 217402, A	c 157	20	1.0	5158	17	US-10-275-933-11	Sequence 11, Appl
C 85	20	1.0	440	12	US-09-925-065A-478249	Sequence 478249, A	c 158	20	1.0	5571	17	US-10-221-613-206	Sequence 206, App
C 86	20	1.0	464	12	US-09-925-065A-829462	Sequence 829462, A	c 159	20	1.0	5571	18	US-10-221-714A-202	Sequence 206, App
C 87	20	1.0	470	18	US-10-424-599-48845	Sequence 48845, A	c 160	20	1.0	5986	15	US-10-240-453-272	Sequence 272, App
C 88	20	1.0	496	12	US-09-925-065A-528958	Sequence 528958, A	c 161	20	1.0	6458	15	US-10-231-778-7	Sequence 7, Appl
C 89	20	1.0	499	12	US-09-925-065A-478250	Sequence 478250, A	c 162	20	1.0	6876	15	US-10-240-589C-118	Sequence 118, App
C 90	20	1.0	499	12	US-09-925-065A-478251	Sequence 478251, A	c 163	20	1.0	6876	15	US-10-311-455-1737	Sequence 1737, App
C 91	20	1.0	500	18	US-10-424-599-131068	Sequence 131068, A	c 164	20	1.0	8662	15	US-10-240-485-189	Sequence 189, App
C 92	20	1.0	513	21	US-10-696-635-1977	Sequence 1977, App	c 165	20	1.0	10425	24	US-11-097-143-35281	Sequence 35281, A
C 93	20	1.0	524	12	US-09-925-065A-554898	Sequence 554898, A	c 166	20	1.0	10891	25	US-10-311-455-437	Sequence 437, App
C 94	20	1.0	536	12	US-09-925-065A-242709	Sequence 242709, A	c 167	20	1.0	12893	20	US-10-719-993-7006	Sequence 7006, App
C 95	20	1.0	536	12	US-09-925-065A-242710	Sequence 242710, A	c 168	20	1.0	12893	21	US-10-741-600-17932	Sequence 17932, A
C 96	20	1.0	541	19	US-10-021-323-11946	Sequence 11946, A	c 169	20	1.0	12939	15	US-10-311-455-1487	Sequence 1487, App
C 97	20	1.0	544	12	US-09-925-065A-161404	Sequence 161404, A	c 170	20	1.0	16918	15	US-10-311-455-1590	Sequence 1590, App
C 98	20	1.0	555	12	US-09-925-065A-664027	Sequence 664027, A	c 171	20	1.0	22660	24	US-11-097-143-11791	Sequence 11791, A
C 99	20	1.0	564	20	US-10-425-115-35479	Sequence 35479, A	c 172	20	1.0	50657	19	US-10-322-281-601	Sequence 601, App
C 100	20	1.0	570	12	US-09-925-065A-552223	Sequence 552223, A	c 173	20	1.0	60604	18	US-10-300-263-11	Sequence 11, Appl
C 101	20	1.0	570	13	US-10-027-632-225521	Sequence 225521, A	c 174	20	1.0	67883	22	US-10-737-082-66	Sequence 66, Appl
C 102	20	1.0	570	13	US-10-027-632-225521	Sequence 225521, A	c 175	20	1.0	67883	22	US-10-765-790-66	Sequence 66, Appl
C 103	20	1.0	572	13	US-10-027-632-225521	Sequence 225521, A	c 176	20	1.0	77777	19	US-10-318-389-4	Sequence 4, Appl
C 104	20	1.0	572	13	US-10-027-632-220249	Sequence 220249, A	c 177	20	1.0	112754	13	US-10-087-192-28	Sequence 28, Appl
C 105	20	1.0	584	17	US-10-027-632-220249	Sequence 220249, A	c 177	20	1.0	112754	13	US-10-087-192-28	Sequence 28, Appl
C 106	20	1.0	585	12	US-09-925-065A-698635	Sequence 698635, A	c 178	20	1.0	122937	21	US-10-322-281-694	Sequence 694, App
C 107	20	1.0	592	12	US-09-925-065A-417816	Sequence 417816, A	c 179	20	1.0	160771	19	US-10-450-826-86	Sequence 86, Appl
C 108	20	1.0	596	12	US-09-925-065A-889953	Sequence 889953, A	c 180	20	1.0	172048	22	US-10-756-149-2157	Sequence 2157, App
C 109	20	1.0	596	12	US-09-925-065A-889954	Sequence 889954, A	c 181	20	1.0	204621	13	US-10-087-192-958	Sequence 958, App
C 110	20	1.0	599	22	US-10-972-075-42702	Sequence 42702, A	c 182	20	1.0	260803	19	US-10-388-838-84	Sequence 84, Appl
C 111	20	1.0	601	12	US-09-925-065A-739335	Sequence 739335, A	c 183	20	1.0	290367	20	US-10-719-993-6887	Sequence 6887, App
C 112	20	1.0	604	12	US-09-925-065A-9411524	Sequence 9411524, A	c 184	20	1.0	721377	21	US-10-461-862-163	Sequence 163, App
C 113	20	1.0	604	12	US-09-925-065A-955708	Sequence 955708, A	c 185	20	1.0	1980090	20	US-10-719-993-6815	Sequence 6815, App
C 114	20	1.0	620	12	US-09-925-065A-460954	Sequence 460954, A	c 186	20	1.0	1980090	21	US-10-741-600-17676	Sequence 17676, A
C 115	20	1.0	621	12	US-09-925-065A-807557	Sequence 807557, A	c 187	19	0.9	100	21	US-10-481-613-200	Sequence 200, App
C 116	20	1.0	623	12	US-09-925-065A-939570	Sequence 939570, A	c 188	19	0.9	100	21	US-10-481-613-205	Sequence 205, App
C 117	20	1.0	628	13	US-10-027-632-24648	Sequence 24648, A	c 189	19	0.9	103	9	US-09-974-300-7318	Sequence 7318, App
C 118	20	1.0	628	17	US-10-027-632-24648	Sequence 24648, A	c 190	19	0.9	153	20	US-10-425-115-96163	Sequence 96163, A
C 119	20	1.0	633	12	US-09-925-065A-718990	Sequence 718990, A	c 191	19	0.9	168	20	US-10-425-115-177493	Sequence 177493, A
C 120	20	1.0	633	12	US-09-925-065A-718991	Sequence 718991, A	c 192	19	0.9	176	20	US-10-425-115-176814	Sequence 176814, A
C 121	20	1.0	633	12	US-09-925-065A-718992	Sequence 718992, A	c 193	19	0.9	201	20	US-10-719-993-36513	Sequence 36513, A
C 122	20	1.0	633	12	US-09-925-065A-718993	Sequence 718993, A	c 194	19	0.9	201	20	US-10-719-993-36514	Sequence 36514, A
C 123	20	1.0	641	12	US-09-925-065A-112512	Sequence 112512, A	c 195	19	0.9	201	21	US-10-741-600-54099	Sequence 54099, A
C 124	20	1.0	645	13	US-10-027-632-257500	Sequence 257500, A	c 196	19	0.9	232	17	US-10-062-674-382	Sequence 382, App
C 125	20	1.0	645	13	US-10-027-632-257501	Sequence 257501, A	c 197	19	0.9	252	18	US-10-424-599-18438	Sequence 18438, A
C 126	20	1.0	645	17	US-10-027-632-257501	Sequence 257501, A	c 198	19	0.9	265	18	US-10-424-599-67157	Sequence 67157, A
C 127	20	1.0	645	17	US-10-027-632-257501	Sequence 257501, A	c 199	19	0.9	277	19	US-10-021-323-7446	Sequence 7446, App
C 128	20	1.0	664	9	US-09-811-284-88	Sequence 88, Appl	c 200	19	0.9	281	12	US-09-925-065A-571495	Sequence 571495, A
C 129	20	1.0	825	17	US-10-282-122A-18058	Sequence 18058, A	c 201	19	0.9	284	18	US-10-424-599-121258	Sequence 121258, A
C 130	20	1.0	851	20	US-10-363-345A-24341	Sequence 24341, A	c 202	19	0.9	285	18	US-10-424-599-111677	Sequence 111677, A
C 131	20	1.0	851	20	US-10-363-345A-24342	Sequence 24342, A	c 203	19	0.9	287	18	US-10-424-599-98985	Sequence 98985, A
C 132	20	1.0	851	21	US-10-363-483A-24341	Sequence 24341, A	c 204	19	0.9	288	20	US-10-424-599-182745	Sequence 182745, A
C 133	20	1.0	851	21	US-10-363-483A-24342	Sequence 24342, A	c 205	19	0.9	325	18	US-10-424-599-113855	Sequence 113855, A
C 134	20	1.0	887	19	US-10-437-963-1670	Sequence 1670, App	c 206	19	0.9	330	20	US-10-425-115-107398	Sequence 107398, A
C 135	20	1.0	888	18	US-10-425-114-16866	Sequence 16866, A	c 207	19	0.9	336	18	US-10-424-599-72226	Sequence 72226, A
C 136	20	1.0	933	21	US-10-956-157-1835	Sequence 1835, App	c 208	19	0.9	340	18	US-10-424-599-57581	Sequence 57581, A
C 137	20	1.0	953	21	US-10-956-157-1835	Sequence 1835, App	c 209	19	0.9	342	20	US-10-425-115-50582	Sequence 50582, A
C 138	20	1.0	968	17	US-10-275-933-12	Sequence 12, Appl	c 210	19	0.9	352	9	US-09-867-701-5104	Sequence 5104, App
C 139	20	1.0	1228	14	US-10-278-173-174	Sequence 174, App	c 211	19	0.9	352	9	US-09-960-352-10129	Sequence 10129, A
C 140	20	1.0	1228	14	US-10-286-264-165	Sequence 165, App	c 212	19	0.9	355	18	US-10-424-599-93610	Sequence 93610, A
C 141	20	1.0	1400	21	US-10-956-157-9394	Sequence 9394, App	c 213	19	0.9	355	20	US-10-357-930-61316	Sequence 61316, A
C 142	20	1.0	1560	9	US-09-938-842A-4778	Sequence 4778, App	c 214	19	0.9	381	20	US-10-357-930-61920	Sequence 61920, A
C 143	20	1.0	1560	11	US-09-938-842A-4778	Sequence 4778, App	c 215	19	0.9	389	10	US-09-918-995-16487	Sequence 16487, A
C 144	20	1.0	1562	19	US-10-437-963-67355	Sequence 67355, A	c 216	19	0.9	396	19	US-10-437-963-3553	Sequence 3553, App
C 145	20	1.0	1645	9	US-09-938-842A-4593	Sequence 4593, App	c 217	19	0.9	398	19	US-10-021-323-7863	Sequence 7863, App
C 146	20	1.0	1645	11	US-09-938-842A-4593	Sequence 4593, App	c 218	19	0.9	400	20	US-10-425-115-58471	Sequence 58471, A
C 147	20	1.0	1945	18	US-10-425-114-10982	Sequence 10982, A	c 219	19	0.9	403	21	US-10-487-804-69	Sequence 69, Appl
C 148	20	1.0	2000	9	US-09-938-842A-3204	Sequence 3204, App	c 220	19	0.9	403	21	US-10-487-804-315	Sequence 315, App
C 149	20	1.0	2000	11	US-09-938-842A-3204	Sequence 3204, App	c 221	19	0.9	403	21	US-10-487-901-6430	Sequence 6430, App
C 150	20	1.0	2482	18	US-10-424-599-57637	Sequence 57637, A	c 222	19	0.9	405	10	US-09-918-995-5353	Sequence 5353, App
C 151	20	1.0	2853	17	US-10-108-260A-601	Sequence 601, App	c 223	19	0.9	411	20	US-10-425-115-25050	Sequence 25050, A
C 152	20	1.0	3230	24	US-11-097-143-16045	Sequence 16045, A	c 224	19	0.9	413	20	US-10-357-930-60973	Sequence 60973, A
C 153	20	1.0	3853	24	US-11-097-143-36403	Sequence 36403, A	c 225	19	0.9	419	13	US-09-918-995-37284	Sequence 37284, A
							c 226	19	0.9	420	13	US-10-027-632-37090	Sequence 37090, A

227	19	0.9	420	17	US-10-027-632-37090	Sequence 37090, A	C 300	19	0.9	586	12	US-09-925-065A-357250	Sequence 357250,
228	19	0.9	422	13	US-10-027-632-182979	Sequence 182979, A	C 301	19	0.9	591	12	US-09-925-065A-394133	Sequence 394133,
229	19	0.9	422	17	US-10-027-632-182979	Sequence 182979, A	C 302	19	0.9	591	12	US-09-925-065A-582644	Sequence 582644,
230	19	0.9	422	18	US-10-424-599-73762	Sequence 73762, A	C 303	19	0.9	596	18	US-10-425-114-20140	Sequence 20140, A
231	19	0.9	423	20	US-10-425-115-72023	Sequence 72023, A	C 304	19	0.9	596	22	US-10-779-543-16066	Sequence 16066, A
232	19	0.9	436	9	US-09-667-701-10366	Sequence 10366, A	C 305	19	0.9	597	12	US-09-925-065A-710142	Sequence 710142,
233	19	0.9	437	20	US-10-357-930-31929	Sequence 31929, A	C 306	19	0.9	598	13	US-10-027-632-189674	Sequence 189674,
234	19	0.9	437	12	US-09-925-065A-11715	Sequence 11715, A	C 307	19	0.9	598	17	US-10-027-632-189674	Sequence 189674,
235	19	0.9	443	18	US-10-424-599-68803	Sequence 68803, A	C 308	19	0.9	599	12	US-09-925-065A-117058	Sequence 117058,
236	19	0.9	445	10	US-09-918-995-4301	Sequence 4301, Ap	C 309	19	0.9	599	12	US-09-925-065A-251879	Sequence 251879,
237	19	0.9	449	13	US-10-027-632-179707	Sequence 179707, A	C 310	19	0.9	600	12	US-09-925-065A-816783	Sequence 816783,
238	19	0.9	449	17	US-10-027-632-179707	Sequence 179707, A	C 311	19	0.9	600	22	US-10-972-079-11039	Sequence 11039, A
239	19	0.9	452	17	US-09-925-065A-511936	Sequence 511936, A	C 312	19	0.9	600	22	US-10-972-079-30532	Sequence 30532, A
240	19	0.9	452	12	US-09-925-065A-511937	Sequence 511937, A	C 313	19	0.9	600	22	US-10-972-079-37444	Sequence 37444, A
241	19	0.9	452	15	US-10-002-623-430	Sequence 430, App	C 314	19	0.9	600	22	US-10-972-079-79365	Sequence 79365, A
242	19	0.9	457	12	US-09-925-065A-748201	Sequence 748201, A	C 315	19	0.9	600	22	US-10-972-079-80159	Sequence 80159, A
243	19	0.9	457	19	US-10-437-963-70141	Sequence 70141, A	C 316	19	0.9	600	22	US-10-972-079-80160	Sequence 80160, A
244	19	0.9	459	12	US-09-925-065A-772934	Sequence 772934, A	C 317	19	0.9	600	22	US-10-972-079-80160	Sequence 80160, A
245	19	0.9	460	12	US-09-925-065A-129311	Sequence 129311, A	C 318	19	0.9	600	22	US-10-972-079-84309	Sequence 84309, A
246	19	0.9	460	20	US-10-425-115-182449	Sequence 182449, A	C 319	19	0.9	600	22	US-10-972-079-84310	Sequence 84310, A
247	19	0.9	461	9	US-09-084-491A-6	Sequence 6, Appli	C 320	19	0.9	601	12	US-09-925-065A-267915	Sequence 267915,
248	19	0.9	461	13	US-10-102-704-6	Sequence 6, Appli	C 321	19	0.9	601	12	US-09-925-065A-267918	Sequence 267918,
249	19	0.9	461	24	US-11-035-988-6	Sequence 6, Appli	C 322	19	0.9	604	12	US-09-925-065A-826040	Sequence 826040,
250	19	0.9	462	12	US-09-925-065A-834297	Sequence 834297, A	C 323	19	0.9	604	12	US-09-925-065A-826040	Sequence 826040,
251	19	0.9	464	12	US-09-925-065A-129310	Sequence 129310, A	C 324	19	0.9	604	12	US-09-925-065A-862610	Sequence 862610,
252	19	0.9	466	20	US-10-425-115-109276	Sequence 109276, A	C 325	19	0.9	606	12	US-09-925-065A-851536	Sequence 851536,
253	19	0.9	475	20	US-10-425-115-4602	Sequence 408276, A	C 326	19	0.9	607	20	US-10-425-115-133745	Sequence 133745,
254	19	0.9	480	20	US-10-357-930-10737	Sequence 10737, A	C 327	19	0.9	609	12	US-09-925-065A-538515	Sequence 538515,
255	19	0.9	484	12	US-09-925-065A-159258	Sequence 159258, A	C 328	19	0.9	609	12	US-09-925-065A-538516	Sequence 538516,
256	19	0.9	484	12	US-09-925-065A-159259	Sequence 159259, A	C 329	19	0.9	611	12	US-09-925-065A-590449	Sequence 590449,
257	19	0.9	484	12	US-09-925-065A-159260	Sequence 159260, A	C 330	19	0.9	612	13	US-10-027-632-126866	Sequence 126866,
258	19	0.9	484	12	US-09-925-065A-159261	Sequence 159261, A	C 331	19	0.9	612	17	US-10-027-632-126867	Sequence 126867,
259	19	0.9	486	9	US-09-974-300-1974	Sequence 1974, Ap	C 332	19	0.9	612	17	US-10-027-632-126867	Sequence 126867,
260	19	0.9	495	28	US-10-424-599-15675	Sequence 15675, A	C 333	19	0.9	612	18	US-10-424-599-39814	Sequence 39814, A
261	19	0.9	501	22	US-10-724-972A-3290	Sequence 3290, Ap	C 334	19	0.9	614	12	US-09-925-065A-467610	Sequence 467610,
262	19	0.9	507	10	US-09-814-353-18907	Sequence 18907, A	C 335	19	0.9	614	12	US-09-925-065A-467611	Sequence 467611,
263	19	0.9	512	12	US-09-925-065A-261778	Sequence 261778, A	C 336	19	0.9	615	12	US-09-925-065A-526545	Sequence 526545,
264	19	0.9	513	12	US-09-925-065A-840308	Sequence 840308, A	C 337	19	0.9	622	12	US-09-925-065A-670743	Sequence 670743,
265	19	0.9	522	18	US-10-424-599-4360	Sequence 4360, Ap	C 338	19	0.9	623	13	US-10-027-632-276707	Sequence 276707,
266	19	0.9	523	12	US-09-925-065A-482104	Sequence 482104, A	C 339	19	0.9	623	17	US-10-027-632-276707	Sequence 276707,
267	19	0.9	523	18	US-10-424-599-86340	Sequence 86340, A	C 340	19	0.9	624	12	US-09-925-065A-146894	Sequence 146894,
268	19	0.9	528	12	US-09-925-065A-32208	Sequence 32208, A	C 341	19	0.9	625	12	US-09-925-065A-755652	Sequence 755652,
269	19	0.9	530	12	US-09-925-065A-753143	Sequence 753143, A	C 342	19	0.9	625	12	US-09-925-065A-875359	Sequence 875359,
270	19	0.9	533	12	US-09-925-065A-603087	Sequence 603087, A	C 343	19	0.9	627	12	US-09-925-065A-762396	Sequence 762396,
271	19	0.9	541	12	US-09-925-065A-577356	Sequence 577356, A	C 344	19	0.9	628	12	US-09-925-065A-365565	Sequence 365565,
272	19	0.9	541	13	US-10-027-632-63235	Sequence 63235, A	C 345	19	0.9	629	12	US-09-925-065A-365566	Sequence 365566,
273	19	0.9	541	17	US-10-027-632-63235	Sequence 63235, A	C 346	19	0.9	629	12	US-09-925-065A-407635	Sequence 407635,
274	19	0.9	549	18	US-10-424-599-87589	Sequence 87589, A	C 347	19	0.9	629	12	US-09-925-065A-870124	Sequence 870124,
275	19	0.9	564	20	US-10-363-345A-5961	Sequence 5961, Ap	C 348	19	0.9	630	12	US-10-363-345A-39440	Sequence 39440, A
276	19	0.9	564	20	US-10-363-345A-5962	Sequence 5962, Ap	C 349	19	0.9	631	20	US-10-363-345A-39440	Sequence 39440, A
277	19	0.9	564	21	US-10-363-483A-5961	Sequence 5961, Ap	C 350	19	0.9	631	21	US-10-363-483A-39440	Sequence 39440, A
278	19	0.9	564	21	US-10-363-483A-5962	Sequence 5962, Ap	C 351	19	0.9	631	21	US-10-363-483A-39440	Sequence 39440, A
279	19	0.9	565	12	US-09-925-065A-652893	Sequence 652893, A	C 352	19	0.9	633	12	US-09-925-065A-875150	Sequence 875150,
280	19	0.9	566	20	US-10-357-930-51743	Sequence 51743, A	C 353	19	0.9	636	12	US-09-925-065A-81492	Sequence 81492, A
281	19	0.9	568	12	US-09-925-065A-319480	Sequence 319480, A	C 354	19	0.9	636	12	US-09-925-065A-81492	Sequence 81492, A
282	19	0.9	568	12	US-09-925-065A-319481	Sequence 319481, A	C 355	19	0.9	636	12	US-09-925-065A-116798	Sequence 116798,
283	19	0.9	569	12	US-09-925-065A-436614	Sequence 436614, A	C 356	19	0.9	639	12	US-09-925-065A-525225	Sequence 525225,
284	19	0.9	571	12	US-09-925-065A-933026	Sequence 933026, A	C 357	19	0.9	639	12	US-09-925-065A-525226	Sequence 525226,
285	19	0.9	572	12	US-09-925-065A-426657	Sequence 426657, A	C 358	19	0.9	639	12	US-09-925-065A-525228	Sequence 525228,
286	19	0.9	573	12	US-09-925-065A-446871	Sequence 446871, A	C 359	19	0.9	639	12	US-09-925-065A-525229	Sequence 525229,
287	19	0.9	577	12	US-09-925-065A-762693	Sequence 762693, A	C 360	19	0.9	639	12	US-09-925-065A-525229	Sequence 525229,
288	19	0.9	577	20	US-10-425-115-171050	Sequence 171050, A	C 361	19	0.9	640	12	US-09-925-065A-682741	Sequence 682741,
289	19	0.9	578	12	US-09-925-065A-823498	Sequence 823498, A	C 362	19	0.9	640	12	US-09-925-065A-682742	Sequence 682742,
290	19	0.9	578	16	US-10-029-386-6290	Sequence 6290, Ap	C 363	19	0.9	640	12	US-09-925-065A-682743	Sequence 682743,
291	19	0.9	579	12	US-09-925-065A-656786	Sequence 656786, A	C 364	19	0.9	647	12	US-10-437-963-74233	Sequence 74233, A
292	19	0.9	580	12	US-09-925-065A-410834	Sequence 410834, A	C 365	19	0.9	656	12	US-09-925-065A-413343	Sequence 413343,
293	19	0.9	580	12	US-09-925-065A-410836	Sequence 410836, A	C 366	19	0.9	656	12	US-09-925-065A-413344	Sequence 413344,
294	19	0.9	582	12	US-09-925-065A-439092	Sequence 439092, A	C 367	19	0.9	658	12	US-09-925-065A-5440	Sequence 5440, Ap
295	19	0.9	584	12	US-09-925-065A-574172	Sequence 574172, A	C 368	19	0.9	661	13	US-09-925-065A-914163	Sequence 914163,
296	19	0.9	585	12	US-09-925-065A-267914	Sequence 267914, A	C 369	19	0.9	664	13	US-10-027-632-7741	Sequence 7741, Ap
297	19	0.9	585	12	US-09-925-065A-267916	Sequence 267916, A	C 370	19	0.9	664	17	US-10-027-632-7741	Sequence 7741, Ap
298	19	0.9	585	13	US-10-027-632-248035	Sequence 248035, A	C 371	19	0.9	670	13	US-10-027-632-170985	Sequence 170985,
299	19	0.9	585	17	US-10-027-632-248035	Sequence 248035, A	C 372	19	0.9	670	17	US-10-027-632-170985	Sequence 170985,

373	19	0.9	696	12	US-09-925-065A-947173	Sequence 947173, A	C 446	19	0.9	1630	12	US-09-925-065A-711468	Sequence 711468, A
c 374	19	0.9	696	14	US-10-198-846-12804	Sequence 12804, A	447	19	0.9	1665	20	US-10-425-115-49808	Sequence 49808, A
375	19	0.9	702	13	US-10-027-632-159391	Sequence 159391, A	448	19	0.9	1666	22	US-10-491-355-41	Sequence 41, Appl
376	19	0.9	702	13	US-10-027-632-159392	Sequence 159392, A	449	19	0.9	1764	12	US-09-925-065A-696442	Sequence 696442, A
377	19	0.9	702	17	US-10-027-632-159391	Sequence 159391, A	c 450	19	0.9	1764	12	US-09-925-065A-696443	Sequence 696443, A
378	19	0.9	702	17	US-10-027-632-159392	Sequence 159392, A	c 451	19	0.9	1782	18	US-10-149-310-81	Sequence 81, Appl
c 379	19	0.9	705	12	US-09-925-065A-75401	Sequence 75401, A	c 452	19	0.9	1803	9	US-09-956-004-71	Sequence 71, Appl
c 380	19	0.9	705	12	US-09-925-065A-75402	Sequence 75402, A	c 453	19	0.9	1803	9	US-10-808-570-71	Sequence 6, Appl
381	19	0.9	709	12	US-09-925-065A-3486	Sequence 3486, A	c 454	19	0.9	1821	9	US-09-737-178-6	Sequence 6, Appl
382	19	0.9	736	13	US-10-027-632-149323	Sequence 149323, A	c 455	19	0.9	1821	9	US-09-286-488-6	Sequence 6, Appl
383	19	0.9	736	17	US-10-027-632-149323	Sequence 149323, A	c 456	19	0.9	1821	10	US-09-853-079-6	Sequence 6, Appl
384	19	0.9	746	13	US-10-027-632-164736	Sequence 164736, A	c 457	19	0.9	1821	17	US-10-294-443-6	Sequence 6, Appl
385	19	0.9	746	17	US-10-027-632-164736	Sequence 164736, A	c 458	19	0.9	1868	11	US-09-938-842A-5068	Sequence 5068, Ap
386	19	0.9	751	13	US-10-027-632-98953	Sequence 98953, A	c 459	19	0.9	1868	11	US-09-938-842A-5068	Sequence 5068, Ap
387	19	0.9	751	17	US-10-027-632-98953	Sequence 98953, A	c 460	19	0.9	1934	12	US-09-925-065A-680444	Sequence 680444, A
388	19	0.9	762	13	US-10-027-632-151185	Sequence 151185, A	c 461	19	0.9	2135	14	US-10-234-432-16	Sequence 16, Appl
389	19	0.9	762	17	US-10-027-632-151185	Sequence 151185, A	c 462	19	0.9	2639	24	US-11-097-143-1190	Sequence 1190, Ap
390	19	0.9	767	20	US-10-363-345A-8369	Sequence 8369, Ap	c 463	19	0.9	2726	17	US-10-104-047-877	Sequence 877, Ap
c 391	19	0.9	767	20	US-10-363-345A-8370	Sequence 8370, Ap	c 464	19	0.9	3107	15	US-10-172-086-94	Sequence 94, Appl
392	19	0.9	767	21	US-10-363-483A-8369	Sequence 8369, Ap	c 465	19	0.9	3107	15	US-10-311-507-82	Sequence 82, Appl
c 393	19	0.9	789	13	US-10-027-632-168159	Sequence 168159, A	c 466	19	0.9	3107	20	US-10-480-846-94	Sequence 94, Appl
394	19	0.9	789	13	US-10-027-632-168159	Sequence 168159, A	c 467	19	0.9	3374	24	US-11-097-143-37639	Sequence 37639, A
395	19	0.9	789	13	US-10-027-632-168159	Sequence 168159, A	c 468	19	0.9	3948	18	US-10-302-172-125	Sequence 125, App
396	19	0.9	789	17	US-10-027-632-168159	Sequence 168159, A	c 469	19	0.9	4223	9	US-09-737-178-7	Sequence 7, Appl
397	19	0.9	789	17	US-10-027-632-168159	Sequence 168159, A	c 470	19	0.9	4223	9	US-09-737-178-7	Sequence 7, Appl
c 398	19	0.9	794	19	US-10-437-963-23812	Sequence 23812, A	c 471	19	0.9	4223	9	US-09-286-488-7	Sequence 7, Appl
399	19	0.9	810	20	US-10-425-115-124194	Sequence 124194, A	c 472	19	0.9	4223	9	US-09-286-488-7	Sequence 7, Appl
c 400	19	0.9	812	13	US-10-027-632-152589	Sequence 152589, A	c 473	19	0.9	4223	10	US-09-853-079-7	Sequence 7, Appl
c 401	19	0.9	812	13	US-10-027-632-152589	Sequence 152589, A	c 474	19	0.9	4223	10	US-09-853-079-7	Sequence 7, Appl
c 402	19	0.9	812	13	US-10-027-632-152591	Sequence 152591, A	c 475	19	0.9	4223	17	US-10-294-443-7	Sequence 7, Appl
c 403	19	0.9	812	13	US-10-027-632-152591	Sequence 152591, A	c 476	19	0.9	4223	17	US-10-294-443-7	Sequence 7, Appl
c 404	19	0.9	812	17	US-10-027-632-152590	Sequence 152590, A	c 477	19	0.9	4223	17	US-10-294-443-45	Sequence 45, Appl
c 405	19	0.9	812	17	US-10-027-632-152591	Sequence 152591, A	c 478	19	0.9	4223	17	US-10-294-443-45	Sequence 45, Appl
406	19	0.9	856	24	US-10-425-114-6864	Sequence 6864, Ap	c 479	19	0.9	5129	24	US-11-097-143-1189	Sequence 1189, Ap
c 407	19	0.9	856	24	US-11-097-143-12788	Sequence 12788, A	c 480	19	0.9	5338	17	US-10-788-792-25	Sequence 25, Appl
c 408	19	0.9	879	18	US-10-424-599-94162	Sequence 94162, A	c 481	19	0.9	5442	15	US-10-221-613-242	Sequence 242, App
c 409	19	0.9	879	20	US-10-425-115-173241	Sequence 173241, A	c 482	19	0.9	5569	24	US-11-097-143-12787	Sequence 12787, A
c 410	19	0.9	899	19	US-10-437-963-27088	Sequence 27088, A	c 483	19	0.9	5807	15	US-10-311-455-1418	Sequence 1418, Ap
c 411	19	0.9	930	22	US-10-724-972A-3583	Sequence 3583, Ap	c 484	19	0.9	5807	15	US-10-311-455-1418	Sequence 1418, Ap
c 412	19	0.9	949	20	US-10-425-115-16816	Sequence 16816, A	c 485	19	0.9	6126	15	US-10-311-455-1163	Sequence 1163, Ap
c 413	19	0.9	987	17	US-10-027-632-325426	Sequence 325426, A	c 486	19	0.9	6240	15	US-10-311-455-1163	Sequence 1163, Ap
c 414	19	0.9	987	17	US-10-027-632-325426	Sequence 325426, A	c 487	19	0.9	6240	15	US-10-311-455-1163	Sequence 1163, Ap
c 415	19	0.9	1002	18	US-10-425-114-13976	Sequence 12976, A	c 488	19	0.9	6240	15	US-10-240-485-8	Sequence 8, Appl
c 416	19	0.9	1033	9	US-09-770-445-188	Sequence 188, App	c 489	19	0.9	6270	15	US-10-311-455-1846	Sequence 1846, Ap
c 417	19	0.9	1040	14	US-10-278-173-157	Sequence 157, App	c 490	19	0.9	6837	10	US-08-928-847B-49	Sequence 49, Appl
c 418	19	0.9	1040	15	US-10-278-536-209	Sequence 209, App	c 491	19	0.9	6866	15	US-10-311-455-640	Sequence 640, App
c 419	19	0.9	1040	18	US-10-412-699B-341	Sequence 341, App	c 492	19	0.9	6988	15	US-10-311-455-2414	Sequence 2414, Ap
c 420	19	0.9	1044	18	US-10-451-337-7	Sequence 7, Appl	c 493	19	0.9	7058	17	US-10-257-166-133	Sequence 133, App
c 421	19	0.9	1044	20	US-10-474-792-179	Sequence 179, App	c 494	19	0.9	7083	24	US-11-097-143-1246	Sequence 1246, Ap
c 422	19	0.9	1078	12	US-09-925-065A-69703	Sequence 69703, A	c 495	19	0.9	7322	14	US-10-198-846-13528	Sequence 13528, A
c 423	19	0.9	1090	20	US-10-425-115-49809	Sequence 49809, A	c 496	19	0.9	7522	15	US-10-239-676-6	Sequence 6, Appl
c 424	19	0.9	1096	18	US-10-424-599-71266	Sequence 71266, A	c 497	19	0.9	7544	14	US-10-239-676-6	Sequence 6, Appl
c 425	19	0.9	1111	16	US-10-252-157-111	Sequence 111, App	c 498	19	0.9	7544	14	US-10-240-453-14	Sequence 14, Appl
c 426	19	0.9	1114	13	US-10-027-632-119019	Sequence 119019, A	c 499	19	0.9	8103	15	US-10-311-455-1634	Sequence 1634, Ap
c 427	19	0.9	1114	17	US-10-027-632-119019	Sequence 119019, A	c 500	19	0.9	8168	15	US-10-311-455-901	Sequence 901, App
c 428	19	0.9	1128	13	US-10-027-632-119513	Sequence 119513, A	c 501	19	0.9	8168	15	US-10-311-455-901	Sequence 901, App
c 429	19	0.9	1128	17	US-10-027-632-119513	Sequence 119513, A	c 502	19	0.9	8168	15	US-10-311-455-902	Sequence 902, App
c 430	19	0.9	1145	13	US-10-027-632-259574	Sequence 259574, A	c 503	19	0.9	8168	18	US-10-240-454-23	Sequence 23, Appl
c 431	19	0.9	1145	17	US-10-027-632-259574	Sequence 259574, A	c 504	19	0.9	8168	18	US-10-240-454-24	Sequence 24, Appl
c 432	19	0.9	1172	17	US-10-369-493-29023	Sequence 29023, A	c 505	19	0.9	8530	15	US-10-311-455-405	Sequence 405, App
c 433	19	0.9	1253	12	US-10-424-599-37287	Sequence 37287, A	c 506	19	0.9	8758	15	US-10-311-455-1091	Sequence 1091, Ap
c 434	19	0.9	1283	18	US-09-925-065A-692044	Sequence 692044, A	c 507	19	0.9	8876	15	US-10-311-455-2049	Sequence 2049, Ap
c 435	19	0.9	1354	20	US-10-425-115-61774	Sequence 61774, A	c 508	19	0.9	8915	24	US-11-097-143-1713	Sequence 1713, A
c 436	19	0.9	1421	12	US-09-925-065A-727205	Sequence 727205, A	c 509	19	0.9	9320	24	US-11-097-143-1713	Sequence 1713, A
c 437	19	0.9	1450	19	US-10-437-963-52708	Sequence 52708, A	c 510	19	0.9	9728	15	US-10-311-455-1876	Sequence 1876, Ap
c 438	19	0.9	1451	15	US-10-172-086-63	Sequence 63, Appl	c 511	19	0.9	9914	9	US-09-764-847-1558	Sequence 1558, Ap
c 439	19	0.9	1451	19	US-10-311-507-23	Sequence 23, Appl	c 512	19	0.9	9914	14	US-10-092-154-1558	Sequence 1558, Ap
c 440	19	0.9	1451	20	US-10-480-846-63	Sequence 63, Appl	c 513	19	0.9	9963	15	US-10-311-455-668	Sequence 668, App
c 441	19	0.9	1470	18	US-10-424-599-66851	Sequence 66851, A	c 514	19	0.9	10528	15	US-10-311-455-308	Sequence 308, App
c 442	19	0.9	1508	12	US-09-925-065A-698799	Sequence 698799, A	c 515	19	0.9	11049	16	US-10-240-589C-30	Sequence 30, Appl
c 443	19	0.9	1559	18	US-10-424-599-21619	Sequence 21619, A	c 516	19	0.9	11670	16	US-10-240-452-25	Sequence 25, Appl
c 444	19	0.9	1581	21	US-10-764-420-2631	Sequence 2631, Ap	c 517	19	0.9	12816	24	US-11-097-143-28519	Sequence 28519, A
c 445	19	0.9	1619	18	US-10-424-599-8667	Sequence 8667, Ap	c 518	19	0.9	12986	18	US-10-221-714A-276	Sequence 276, App



c 519	19	0.9	13449	15	US-10-311-455-1358	Sequence 1358, Ap	c 592	19	0.9	168050	22	US-10-939-321-1	Sequence 1, Appli
c 520	19	0.9	14491	20	US-10-473-126-201	Sequence 201, App	c 593	19	0.9	171324	13	US-10-087-192-67	Sequence 67, Appl
c 521	19	0.9	14491	20	US-10-473-126-347	Sequence 347, App	c 594	19	0.9	180227	19	US-10-322-281-308	Sequence 308, App
c 522	19	0.9	15122	15	US-10-311-455-748	Sequence 748, App	c 595	19	0.9	198285	9	US-09-880-107-3814	Sequence 3814, Ap
c 523	19	0.9	15861	15	US-10-311-455-497	Sequence 497, App	c 596	19	0.9	198285	9	US-10-775-169-338	Sequence 338, App
c 524	19	0.9	16127	15	US-10-311-455-718	Sequence 718, App	c 597	19	0.9	198285	22	US-10-756-149-12	Sequence 12, Appl
c 525	19	0.9	16173	15	US-10-240-485-21	Sequence 21, Appl	c 598	19	0.9	203127	22	US-10-741-601-5554	Sequence 5654, Ap
c 526	19	0.9	16688	18	US-10-221-714A-277	Sequence 277, App	c 599	19	0.9	203127	21	US-10-741-600-17666	Sequence 17666, A
c 527	19	0.9	17421	14	US-10-239-676-54	Sequence 54, Appl	c 600	19	0.9	224112	19	US-10-367-094-80	Sequence 80, Appl
c 528	19	0.9	17421	15	US-10-239-676-54	Sequence 56, Appl	c 601	19	0.9	235033	15	US-10-301-844-1	Sequence 1, Appli
c 529	19	0.9	17421	15	US-10-240-453-56	Sequence 56, Appl	c 602	19	0.9	237326	15	US-10-301-844-2	Sequence 2, Appli
c 530	19	0.9	17421	15	US-10-240-485-127	Sequence 127, App	c 603	19	0.9	241805	19	US-10-741-601-5621	Sequence 5621, Ap
c 531	19	0.9	17491	15	US-10-240-485-108	Sequence 108, App	c 604	19	0.9	241805	21	US-10-741-600-17581	Sequence 17581, A
c 532	19	0.9	17534	17	US-10-257-166-108	Sequence 166, App	c 605	19	0.9	277616	19	US-10-367-094-83	Sequence 83, Appl
c 533	19	0.9	17721	15	US-10-311-455-1701	Sequence 1701, Ap	c 606	19	0.9	290547	19	US-10-367-094-77	Sequence 77, Appl
c 534	19	0.9	17970	19	US-10-433-793-64	Sequence 64, Appl	c 607	19	0.9	340905	18	US-10-271-416-1	Sequence 1, Appli
c 535	19	0.9	18133	15	US-10-311-455-913	Sequence 913, App	c 608	19	0.9	330973	13	US-10-087-193-1498	Sequence 1498, Ap
c 536	19	0.9	18133	17	US-10-257-166-99	Sequence 99, Appl	c 609	19	0.9	368004	9	US-09-949-654-3	Sequence 3, Appli
c 537	19	0.9	18357	19	US-10-433-793-114	Sequence 114, App	c 610	19	0.9	410846	21	US-10-481-613-1	Sequence 1, Appli
c 538	19	0.9	21500	13	US-10-087-192-169	Sequence 169, App	c 611	19	0.9	580073	16	US-10-205-220-1	Sequence 1, Appli
c 539	19	0.9	25179	19	US-10-322-281-277	Sequence 277, App	c 612	19	0.9	653122	13	US-10-087-192-226	Sequence 226, App
c 540	19	0.9	28118	17	US-10-282-174-402	Sequence 402, App	c 613	19	0.9	1691139	14	US-10-067-514-1	Sequence 1, Appli
c 541	19	0.9	28118	17	US-10-282-174-403	Sequence 403, App	c 614	19	0.9	1691139	17	US-10-419-723-1	Sequence 1, Appli
c 542	19	0.9	28118	21	US-10-600-009-402	Sequence 402, App	c 615	19	0.9	1931140	22	US-10-868-397-1	Sequence 1, Appli
c 543	19	0.9	28118	21	US-10-600-009-403	Sequence 403, App	c 616	19	0.9	3673778	16	US-10-312-841-1	Sequence 1, Appli
c 544	19	0.9	29222	17	US-10-085-117-349	Sequence 349, App	c 617	19	0.9	3673778	16	US-10-312-841-2	Sequence 2, Appli
c 545	19	0.9	29222	21	US-10-482-823-3	Sequence 3, Appli	c 618	18	0.9	25	24	US-11-036-317-35082	Sequence 35082, A

665	18	0.9	337	18	US-10-424-599-13918	Sequence 13918, A	738	18	0.9	418	20	US-10-357-930-2244	Sequence 2244, Ap
666	18	0.9	337	20	US-10-425-115-113420	Sequence 113420, A	739	18	0.9	420	20	US-10-425-115-181784	Sequence 181784, A
667	18	0.9	339	20	US-10-357-930-12918	Sequence 12918, A	c 740	18	0.9	424	20	US-10-425-115-52807	Sequence 52807, A
c 668	18	0.9	339	22	US-10-724-972A-3176	Sequence 3176, Ap	741	18	0.9	425	18	US-10-424-599-115705	Sequence 115705, A
669	18	0.9	341	20	US-10-425-115-138884	Sequence 138884, A	c 742	18	0.9	426	10	US-09-814-353-18496	Sequence 18496, A
670	18	0.9	344	19	US-10-437-963-96105	Sequence 96105, A	c 743	18	0.9	428	13	US-10-027-632-273956	Sequence 273956, A
c 671	18	0.9	347	18	US-10-424-599-103550	Sequence 103550, A	c 744	18	0.9	428	17	US-10-027-632-273956	Sequence 273956, A
672	18	0.9	349	18	US-10-424-599-132938	Sequence 132938, A	c 745	18	0.9	428	20	US-10-357-930-14207	Sequence 14207, A
673	18	0.9	353	10	US-09-803-719-1218	Sequence 1218, Ap	c 746	18	0.9	429	12	US-09-925-065A-148388	Sequence 148388, A
674	18	0.9	353	22	US-10-779-543-14488	Sequence 14488, A	c 747	18	0.9	429	12	US-09-925-065A-148389	Sequence 148389, A
675	18	0.9	354	20	US-10-425-115-26048	Sequence 26048, A	c 748	18	0.9	429	12	US-09-925-065A-651275	Sequence 651275, A
676	18	0.9	355	18	US-10-424-599-84294	Sequence 84294, A	c 749	18	0.9	429	19	US-10-437-963-50818	Sequence 50818, A
677	18	0.9	357	18	US-10-424-599-62329	Sequence 62329, A	c 750	18	0.9	430	10	US-09-918-995-6348	Sequence 6348, Ap
678	18	0.9	359	15	US-10-046-955-23	Sequence 23, Appl	c 751	18	0.9	430	10	US-10-424-599-68040	Sequence 68040, A
c 679	18	0.9	360	12	US-09-925-065A-49040	Sequence 49040, A	c 752	18	0.9	431	20	US-10-425-115-127998	Sequence 127998, A
c 680	18	0.9	365	18	US-10-424-599-93941	Sequence 93941, A	c 753	18	0.9	432	9	US-09-770-423-114	Sequence 114, App
c 681	18	0.9	366	10	US-09-918-995-29907	Sequence 29907, A	c 754	18	0.9	434	9	US-09-728-445-694	Sequence 694, App
682	18	0.9	366	20	US-10-357-930-3749	Sequence 3749, Ap	c 755	18	0.9	434	9	US-09-960-352-3525	Sequence 3525, Ap
683	18	0.9	367	20	US-10-357-930-11413	Sequence 11413, A	c 755	18	0.9	434	22	US-10-964-549-694	Sequence 694, App
684	18	0.9	368	11	US-09-876-143-618	Sequence 618, App	c 756	18	0.9	435	10	US-09-814-353-13531	Sequence 13531, A
685	18	0.9	369	9	US-09-974-300-3818	Sequence 3818, Ap	c 757	18	0.9	435	12	US-09-925-065A-631751	Sequence 631751, A
c 686	18	0.9	375	18	US-10-424-599-128515	Sequence 128515, A	c 758	18	0.9	435	12	US-09-925-065A-631752	Sequence 631752, A
c 687	18	0.9	377	12	US-09-925-065A-134778	Sequence 134778, A	c 759	18	0.9	435	13	US-10-027-632-277919	Sequence 277919, A
c 688	18	0.9	377	20	US-10-425-115-1910	Sequence 1910, Ap	c 761	18	0.9	439	17	US-10-027-632-277919	Sequence 277919, A
c 689	18	0.9	379	18	US-10-424-599-102184	Sequence 102184, A	c 762	18	0.9	441	10	US-09-814-353-13628	Sequence 13628, A
c 690	18	0.9	382	19	US-10-674-124A-18472	Sequence 18472, A	c 763	18	0.9	444	10	US-09-814-353-1520	Sequence 1520, Ap
c 691	18	0.9	382	20	US-10-425-115-638	Sequence 638, App	c 764	18	0.9	444	10	US-09-814-353-7879	Sequence 7879, Ap
c 692	18	0.9	384	9	US-09-770-791-102	Sequence 102, App	c 765	18	0.9	445	9	US-09-983-965-3978	Sequence 3978, Ap
c 693	18	0.9	384	19	US-10-437-963-29145	Sequence 29145, A	c 766	18	0.9	445	12	US-09-925-065A-205717	Sequence 205717, A
c 694	18	0.9	384	20	US-10-425-115-118891	Sequence 118891, A	c 767	18	0.9	446	10	US-09-814-353-1503	Sequence 1503, Ap
c 695	18	0.9	385	10	US-09-814-353-878	Sequence 878, App	c 768	18	0.9	446	10	US-09-814-353-7862	Sequence 7862, Ap
c 696	18	0.9	385	10	US-09-814-353-7249	Sequence 7249, Ap	c 769	18	0.9	446	15	US-10-071-510-7	Sequence 7, Appli
c 697	18	0.9	389	18	US-09-814-353-24544	Sequence 24544, A	c 770	18	0.9	447	20	US-10-357-930-5038	Sequence 5038, Ap
c 698	18	0.9	389	20	US-10-425-115-144448	Sequence 144448, A	c 771	18	0.9	448	9	US-09-777-564-1170	Sequence 1170, Ap
c 699	18	0.9	390	9	US-09-777-564-977	Sequence 977, App	c 772	18	0.9	448	14	US-10-015-219-1170	Sequence 1170, Ap
c 700	18	0.9	390	9	US-09-777-564-1415	Sequence 1415, Ap	c 773	18	0.9	448	12	US-10-021-323-10901	Sequence 10901, A
c 701	18	0.9	390	14	US-10-015-219-977	Sequence 977, App	c 774	18	0.9	449	12	US-09-925-065A-522033	Sequence 522033, A
c 702	18	0.9	390	14	US-10-015-219-1415	Sequence 1415, Ap	c 775	18	0.9	452	17	US-10-242-535A-42236	Sequence 42236, A
c 703	18	0.9	390	18	US-10-424-599-14981	Sequence 14981, A	c 776	18	0.9	452	18	US-10-085-783A-42236	Sequence 42236, A
704	18	0.9	391	20	US-10-357-930-37444	Sequence 37444, A	c 777	18	0.9	456	20	US-10-357-930-9271	Sequence 9271, Ap
705	18	0.9	393	10	US-09-814-353-813	Sequence 813, App	c 778	18	0.9	462	10	US-09-918-995-13913	Sequence 13913, A
706	18	0.9	393	10	US-09-814-353-7185	Sequence 7185, Ap	c 779	18	0.9	462	10	US-09-814-353-894	Sequence 894, App
707	18	0.9	394	10	US-09-814-353-621	Sequence 621, App	c 780	18	0.9	462	10	US-09-814-353-7265	Sequence 7265, Ap
708	18	0.9	394	10	US-09-814-353-6998	Sequence 6998, Ap	c 781	18	0.9	463	10	US-09-814-353-1521	Sequence 1521, Ap
709	18	0.9	396	20	US-10-357-930-1325	Sequence 1325, App	c 782	18	0.9	463	10	US-09-814-353-7880	Sequence 7880, Ap
c 710	18	0.9	397	9	US-09-777-564-1148	Sequence 1148, Ap	c 783	18	0.9	463	12	US-09-925-065A-629368	Sequence 629368, A
c 711	18	0.9	397	14	US-10-015-219-1148	Sequence 1148, Ap	c 784	18	0.9	463	15	US-10-071-510-10	Sequence 10, Appli
c 712	18	0.9	398	9	US-09-777-564-1345	Sequence 1345, Ap	c 785	18	0.9	464	9	US-10-357-930-30474	Sequence 30474, A
c 713	18	0.9	398	14	US-10-015-219-1345	Sequence 1345, Ap	c 786	18	0.9	464	9	US-09-864-761-5329	Sequence 5329, Ap
c 714	18	0.9	399	18	US-10-424-599-8305	Sequence 8305, Ap	c 787	18	0.9	464	20	US-10-425-115-41771	Sequence 41771, A
715	18	0.9	399	18	US-10-424-599-29877	Sequence 29877, A	c 788	18	0.9	465	9	US-09-777-564-1023	Sequence 1023, Ap
716	18	0.9	400	20	US-10-425-115-177601	Sequence 177601, A	c 789	18	0.9	465	9	US-09-777-564-1462	Sequence 1462, Ap
717	18	0.9	400	20	US-10-357-930-47311	Sequence 47311, A	c 790	18	0.9	465	14	US-10-015-219-1023	Sequence 1023, Ap
c 718	18	0.9	401	12	US-09-925-065A-783137	Sequence 783137, A	c 791	18	0.9	465	14	US-10-015-219-1462	Sequence 1462, Ap
c 719	18	0.9	401	12	US-09-925-065A-783138	Sequence 783138, A	c 792	18	0.9	466	10	US-09-814-353-1449	Sequence 1449, Ap
c 720	18	0.9	402	9	US-09-880-107-1364	Sequence 1364, Ap	c 793	18	0.9	466	10	US-09-814-353-7810	Sequence 7810, Ap
c 721	18	0.9	404	10	US-09-918-995-8805	Sequence 8805, Ap	c 794	18	0.9	466	10	US-09-814-353-1419	Sequence 1419, Ap
c 722	18	0.9	406	12	US-09-925-065A-651276	Sequence 651276, A	c 795	18	0.9	467	10	US-09-814-353-7781	Sequence 7781, Ap
c 723	18	0.9	406	20	US-10-425-115-164311	Sequence 164311, A	c 796	18	0.9	468	20	US-10-357-930-56219	Sequence 56219, A
724	18	0.9	407	9	US-09-770-423-660	Sequence 660, App	c 797	18	0.9	469	10	US-09-814-353-13634	Sequence 13634, A
c 725	18	0.9	408	10	US-09-918-998-3718	Sequence 3718, Ap	c 798	18	0.9	469	18	US-10-424-599-22509	Sequence 22509, A
c 726	18	0.9	408	19	US-10-021-323-11090	Sequence 11090, A	c 799	18	0.9	470	9	US-09-783-590-12453	Sequence 12453, A
727	18	0.9	408	20	US-10-425-115-123610	Sequence 123610, A	c 800	18	0.9	470	10	US-09-814-353-617	Sequence 617, App
728	18	0.9	409	10	US-09-918-995-3982	Sequence 3982, Ap	c 801	18	0.9	470	10	US-09-814-353-6994	Sequence 6994, Ap
c 729	18	0.9	409	10	US-09-814-353-17309	Sequence 17309, A	c 802	18	0.9	470	20	US-10-357-930-32585	Sequence 32585, A
730	18	0.9	410	12	US-09-925-065A-638112	Sequence 638112, A	c 803	18	0.9	470	20	US-10-357-930-34070	Sequence 34070, A
731	18	0.9	410	12	US-09-925-065A-638113	Sequence 638113, A	c 804	18	0.9	470	20	US-10-357-930-41511	Sequence 41511, A
732	18	0.9	410	18	US-10-424-599-61494	Sequence 61494, A	c 805	18	0.9	472	12	US-09-925-065A-450855	Sequence 450855, A
c 733	18	0.9	410	20	US-10-357-930-56415	Sequence 56415, A	c 806	18	0.9	473	18	US-10-424-599-34978	Sequence 34978, A
734	18	0.9	415	10	US-09-814-353-2907	Sequence 2907, Ap	c 807	18	0.9	473	18	US-09-925-065A-165096	Sequence 165096, A
c 735	18	0.9	415	10	US-09-814-353-9236	Sequence 9236, Ap	c 808	18	0.9	475	12	US-09-925-065A-165096	Sequence 165096, A
c 736	18	0.9	415	18	US-10-424-599-112318	Sequence 112318, A	c 809	18	0.9	476	22	US-10-972-079-858	Sequence 858, App
c 737	18	0.9	416	15	US-10-007-926A-284	Sequence 284, App	c 810	18	0.9	477	10	US-09-814-353-14255	Sequence 14255, A

811	18	0.9	477	13	US-10-027-632-65273	Sequence 65273, A	C 884	18	0.9	510	20	US-10-363-345A-16650	Sequence 16650, A
812	18	0.9	477	13	US-10-027-632-65274	Sequence 65274, A	885	18	0.9	510	21	US-10-363-483A-16649	Sequence 16649, A
813	18	0.9	477	17	US-10-027-632-65273	Sequence 65273, A	886	18	0.9	510	21	US-10-363-483A-16650	Sequence 16650, A
814	18	0.9	477	17	US-10-027-632-65274	Sequence 65274, A	887	18	0.9	511	12	US-09-814-353-14274	Sequence 14274, A
815	18	0.9	477	17	US-10-027-632-65274	Sequence 65274, A	888	18	0.9	511	12	US-09-925-065A-755667	Sequence 755667, A
816	18	0.9	477	17	US-10-242-535A-29901	Sequence 29901, A	889	18	0.9	512	12	US-09-925-065A-320094	Sequence 320094, A
817	18	0.9	477	20	US-10-085-783A-29901	Sequence 29901, A	890	18	0.9	512	12	US-09-925-065A-320094	Sequence 320094, A
818	18	0.9	477	20	US-10-425-115-137159	Sequence 137159, A	891	18	0.9	512	18	US-10-424-599-314	Sequence 314, App
819	18	0.9	478	13	US-09-918-995-35423	Sequence 35423, A	892	18	0.9	512	18	US-10-424-599-314	Sequence 314, App
820	18	0.9	478	13	US-10-027-632-184293	Sequence 184293, A	893	18	0.9	513	10	US-09-814-353-15748	Sequence 15748, A
821	18	0.9	478	17	US-10-027-632-184293	Sequence 184293, A	894	18	0.9	513	10	US-09-814-353-15748	Sequence 15748, A
822	18	0.9	479	18	US-10-424-599-113649	Sequence 113649, A	895	18	0.9	519	10	US-09-814-353-15748	Sequence 15748, A
823	18	0.9	479	20	US-10-357-930-35328	Sequence 35328, A	896	18	0.9	519	10	US-09-814-353-15748	Sequence 15748, A
824	18	0.9	479	20	US-10-357-930-35328	Sequence 35328, A	897	18	0.9	519	10	US-09-814-353-15748	Sequence 15748, A
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826	18	0.9	480	10	US-09-814-353-12768	Sequence 12768, A	899	18	0.9	523	10	US-09-814-353-12768	Sequence 12768, A
827	18	0.9	480	12	US-09-925-065A-474626	Sequence 474626, A	900	18	0.9	523	10	US-09-814-353-12768	Sequence 12768, A
828	18	0.9	480	12	US-09-925-065A-474627	Sequence 474627, A	901	18	0.9	523	10	US-09-814-353-12768	Sequence 12768, A
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830	18	0.9	481	10	US-09-814-353-4944	Sequence 4944, App	903	18	0.9	525	12	US-09-925-065A-522055	Sequence 522055, A
831	18	0.9	481	13	US-10-027-633-193998	Sequence 193998, A	904	18	0.9	525	12	US-09-925-065A-825236	Sequence 825236, A
832	18	0.9	481	17	US-10-027-633-193998	Sequence 193998, A	905	18	0.9	525	12	US-09-925-065A-825236	Sequence 825236, A
833	18	0.9	482	20	US-09-925-065A-130199	Sequence 130199, A	906	18	0.9	526	12	US-09-925-065A-582380	Sequence 582380, A
834	18	0.9	482	20	US-10-357-930-49174	Sequence 49174, A	907	18	0.9	527	12	US-09-925-065A-607331	Sequence 607331, A
835	18	0.9	483	20	US-10-723-860-1395	Sequence 1395, App	908	18	0.9	527	13	US-10-027-632-99300	Sequence 99300, A
836	18	0.9	484	12	US-09-925-065A-83308	Sequence 83308, A	909	18	0.9	527	13	US-10-027-632-99300	Sequence 99300, A
837	18	0.9	485	9	US-09-833-790-58	Sequence 58, App1	910	18	0.9	527	13	US-10-027-632-99300	Sequence 99300, A
838	18	0.9	485	12	US-09-925-065A-350643	Sequence 350643, A	911	18	0.9	528	13	US-10-027-632-276197	Sequence 276197, A
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840	18	0.9	485	12	US-09-925-065A-350645	Sequence 350645, A	913	18	0.9	531	20	US-10-357-930-30497	Sequence 30497, A
841	18	0.9	485	12	US-09-925-065A-350646	Sequence 350646, A	914	18	0.9	531	20	US-10-357-930-30497	Sequence 30497, A
842	18	0.9	486	10	US-09-814-353-13650	Sequence 13650, A	915	18	0.9	531	20	US-10-357-930-30497	Sequence 30497, A
843	18	0.9	488	10	US-09-814-353-1447	Sequence 1447, App	916	18	0.9	531	20	US-10-357-930-30497	Sequence 30497, A
844	18	0.9	488	10	US-09-814-353-1531	Sequence 1531, App	917	18	0.9	533	20	US-10-425-115-86834	Sequence 86834, A
845	18	0.9	488	10	US-09-814-353-7808	Sequence 7808, App	918	18	0.9	533	20	US-10-425-115-86834	Sequence 86834, A
846	18	0.9	488	10	US-09-814-353-7890	Sequence 7890, App	919	18	0.9	533	20	US-10-425-115-86834	Sequence 86834, A
847	18	0.9	488	15	US-10-071-510-9	Sequence 9, App11	920	18	0.9	533	20	US-10-425-115-86834	Sequence 86834, A
848	18	0.9	488	22	US-10-972-079-79086	Sequence 79086, A	921	18	0.9	534	12	US-09-925-065A-893335	Sequence 893335, A
849	18	0.9	490	20	US-10-425-115-83754	Sequence 83754, A	922	18	0.9	535	10	US-09-814-353-13383	Sequence 13383, A
850	18	0.9	490	22	US-10-972-079-857	Sequence 857, App	923	18	0.9	535	10	US-09-814-353-13383	Sequence 13383, A
851	18	0.9	491	12	US-09-925-065A-383591	Sequence 383591, A	924	18	0.9	538	12	US-09-925-065A-309509	Sequence 309509, A
852	18	0.9	491	12	US-09-925-065A-938715	Sequence 938715, A	925	18	0.9	540	13	US-10-027-632-27207	Sequence 27207, A
853	18	0.9	491	20	US-10-723-860-2873	Sequence 2873, App	926	18	0.9	540	13	US-10-027-632-27207	Sequence 27207, A
854	18	0.9	492	10	US-09-814-353-14246	Sequence 14246, A	927	18	0.9	540	13	US-10-027-632-27207	Sequence 27207, A
855	18	0.9	497	10	US-09-814-353-1456	Sequence 1456, App	928	18	0.9	540	13	US-10-027-632-27207	Sequence 27207, A
856	18	0.9	497	10	US-09-814-353-7817	Sequence 7817, App	929	18	0.9	540	13	US-10-027-632-27207	Sequence 27207, A
857	18	0.9	497	15	US-10-071-510-8	Sequence 8, App11	930	18	0.9	540	13	US-10-027-632-27207	Sequence 27207, A
858	18	0.9	497	19	US-10-437-963-85578	Sequence 85578, A	931	18	0.9	540	13	US-10-027-632-27207	Sequence 27207, A
859	18	0.9	498	10	US-09-814-353-1512	Sequence 1512, App	932	18	0.9	541	12	US-09-925-065A-345741	Sequence 345741, A
860	18	0.9	498	10	US-09-814-353-7871	Sequence 7871, App	933	18	0.9	541	12	US-09-925-065A-345741	Sequence 345741, A
861	18	0.9	498	12	US-09-925-065A-566432	Sequence 566432, A	934	18	0.9	541	12	US-09-925-065A-417788	Sequence 417788, A
862	18	0.9	500	20	US-10-425-115-68926	Sequence 68926, A	935	18	0.9	542	10	US-09-814-353-14195	Sequence 14195, A
863	18	0.9	502	17	US-10-242-535A-13950	Sequence 13950, A	936	18	0.9	542	10	US-09-814-353-14195	Sequence 14195, A
864	18	0.9	502	18	US-10-085-783A-13950	Sequence 13950, A	937	18	0.9	542	10	US-09-925-065A-157219	Sequence 157219, A
865	18	0.9	502	20	US-10-425-115-57498	Sequence 57498, A	938	18	0.9	543	12	US-09-925-065A-157219	Sequence 157219, A
866	18	0.9	503	10	US-09-814-353-14202	Sequence 14202, A	939	18	0.9	544	17	US-10-027-632-50544	Sequence 50544, A
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868	18	0.9	503	12	US-09-925-065A-805846	Sequence 805846, A	941	18	0.9	544	17	US-10-027-632-50544	Sequence 50544, A
869	18	0.9	503	12	US-09-814-353-14264	Sequence 14264, A	942	18	0.9	545	12	US-09-925-065A-187853	Sequence 187853, A
870	18	0.9	503	20	US-10-357-930-60821	Sequence 60821, A	943	18	0.9	545	12	US-09-925-065A-187853	Sequence 187853, A
871	18	0.9	504	10	US-09-814-353-13570	Sequence 13570, A	944	18	0.9	546	12	US-09-925-065A-185174	Sequence 185174, A
872	18	0.9	504	18	US-10-424-599-141347	Sequence 141347, A	945	18	0.9	546	12	US-09-925-065A-185175	Sequence 185175, A
873	18	0.9	505	12	US-09-925-065A-420355	Sequence 420355, A	946	18	0.9	546	12	US-09-925-065A-185175	Sequence 185175, A
874	18	0.9	505	12	US-09-925-065A-580184	Sequence 580184, A	947	18	0.9	546	12	US-09-925-065A-285292	Sequence 285292, A
875	18	0.9	505	12	US-09-925-065A-580185	Sequence 580185, A	948	18	0.9	546	12	US-09-925-065A-285292	Sequence 285292, A
876	18	0.9	505	12	US-09-925-065A-580186	Sequence 580186, A	949	18	0.9	547	12	US-09-925-065A-187854	Sequence 187854, A
877	18	0.9	505	20	US-10-363-345A-2065	Sequence 2065, App	950	18	0.9	547	12	US-09-925-065A-187854	Sequence 187854, A
878	18	0.9	505	20	US-10-363-345A-2066	Sequence 2066, App	951	18	0.9	547	12	US-09-925-065A-187854	Sequence 187854, A
879	18	0.9	505	21	US-10-363-483A-2066	Sequence 2066, App	952	18	0.9	547	12	US-09-925-065A-187854	Sequence 187854, A
880	18	0.9	505	21	US-10-363-483A-2066	Sequence 2066, App	953	18	0.9	547	12	US-09-925-065A-187854	Sequence 187854, A
881	18	0.9	509	12	US-09-925-065A-556031	Sequence 556031, A	954	18	0.9	548	12	US-09-925-065A-305468	Sequence 305468, A
882	18	0.9	510	19	US-10-021-323-677	Sequence 677, App	955	18	0.9	548	12	US-09-925-065A-305468	Sequence 305468, A
883	18	0.9	510	20	US-10-363-345A-16649	Sequence 16649, A	956	18	0.9	548	12	US-09-925-065A-305468	Sequence 305468, A

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963	18	0.9	558	10	US-09-814-353-14174	Sequence 14174, A	1	CTTCATAGAAGGATGGACCATTTGAAGAATACCTTTCTCTTTCTATTTTCTATTTTATTTGATTTAG	60			
964	18	0.9	558	12	US-09-925-065A-414218	Sequence 414218,						
c 965	18	0.9	559	12	US-09-925-065A-289148	Sequence 289148,	61	AAATCATATTCATTACAAAAGGAAAAAATAATTTTGTATCTCTAAAGTTATTAAC	120			
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c 968	18	0.9	561	9	US-09-777-564-1199	Sequence 1199, Ap						
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971	18	0.9	562	12	US-09-925-065A-297134	Sequence 297134,	121	TTACATTTTCCACACTTCAGTTGCTAGTATTAATTTATCTATTTTATCTAAAGTTTGG	180			
972	18	0.9	562	12	US-09-925-065A-604581	Sequence 604581,						
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c 981	18	0.9	565	12	US-09-925-065A-197135	Sequence 197135,	301	GAATAATAGATCGAATCACAGTTTTCAGTGTAAAGAGGATTTGATATTTGGTCGACATTT	360			
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c 988	18	0.9	570	12	US-09-925-065A-147890	Sequence 147890,						
c 989	18	0.9	570	12	US-09-925-065A-632687	Sequence 632687,	421	TCAACACTTTGTATTAACCGAATAGTATATATCTAGAGCTAGCCCAATACCAAAAATAAA	480			
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993	18	0.9	571	20	US-10-357-930-35240	Sequence 35240, A	481	ATTAAACTCAATTCACAAATTTGAATCTACACCATATCATGCATATATATCAGCAACCTA	540			
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							901	GTCTTTTACCTTTTAAAGAAACCCAACTATTTTCCGGTTGAATTTTGGTTTAACTATTGATTT	960			
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ALIGNMENTS

RESULT 1  
US-10-643-676-1  
; Sequence 1, Application US/10643676  
; Publication No. US20050176946A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Terry  
; APPLICANT: Nuccio, Michael  
; APPLICANT: Hsieh, Tsung-Fu  
; TITLE OF INVENTION: Constitutive promoter from Arabidopsis  
; FILE REFERENCE: A35997-PCT-USA-A (072667, 0188)  
; CURRENT APPLICATION NUMBER: US/10/643, 676  
; CURRENT FILING DATE: 2003-08-19  
; PRIOR APPLICATION NUMBER: PCT/EP02/02894  
; PRIOR FILING DATE: February 14, 2002  
; PRIOR APPLICATION NUMBER: 60/270,779  
; PRIOR FILING DATE: February 22, 2001  
; NUMBER OF SEQ IDS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2030  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-643-676-1

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Db 1081 AGAGGGGATGCGCAAAATCGTAATTAACAAAGGAAAAATAAGGGTGGTTTCCAGTAAGTC 1140  
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RESULT 2  
US-10-643-676-2  
; Sequence 2, Application US/10643676  
; Publication No. US20050176946A1  
; GENERAL INFORMATION:

; APPLICANT: Thomas, Terry  
; APPLICANT: Nuccio, Michael  
; APPLICANT: Heieh, Tzung-Fu  
; TITLE OF INVENTION: Constitutive promoter from Arabidopsis  
; FILE REFERENCE: A35897-PCI--USA-A (072667.0188)  
; CURRENT APPLICATION NUMBER: US/10/643,676  
; CURRENT FILING DATE: 2003-08-19  
; PRIOR APPLICATION NUMBER: PCT/EP02/02894  
; PRIOR FILING DATE: February 14, 2002  
; PRIOR APPLICATION NUMBER: 60/270,779  
; PRIOR FILING DATE: February 22, 2001  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 2042  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; US-10-643-676-2  
  
Query Match 100.0%; Score 2030; DB 22; Length 2042;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2030; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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RESULT 3  
US-09-938-842A-4152  
; Sequence 4152, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 4152  
; LENGTH: 1064  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-4152

Query Match 52.4%; Score 1064; DB 9; Length 1064;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1064; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Qy 1027 ACCGAAAAACAGAAACCGTTATGACGCCAACGAGGCAAGGGGTAAACCGAAAGAGGG 1086  
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Db 121 GATGCGAGAAATCGTAAATTAACAAGAAAAATAAGGGTGGTTTTCAGATAAGTCTGTCTA 180  
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DB 841 TTGGTTTTGTCGTTTTTATAGAAATGAAATATGTAATTTGTTTTTTTCCACAGTAGA 900
QY 1867 TATGTACTATACACATAAGTAACATGGTAGTTTATATAGAGAGAGATTGATTTTTTC 1926
DB 901 TATGTACTATACACATAAGTAACATGGTAGTTTATATAGAGAGAGATTGATTTTTTC 960
QY 1927 GTATATTTCTTTGTCGAAATAAATATGTAAGTAATTTATGTTTATTAATTTGACAGA 1986
DB 961 GTATATTTCTTTGTCGAAATAAATATGTAAGTAATTTATGTTTATTAATTTGACAGA 1020
QY 1987 TTTGTTCCAGTTGAGAAAGTTTAAATTTAGATTAAACACAAAAAG 2030
DB 1021 TTTGTTCCAGTTGAGAAAGTTTAAATTTAGATTAAACACAAAAAG 1064

RESULT 4
US-09-938-842A-4152
; Sequence 4152, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIP300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4152
; LENGTH: 1064
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4152
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Query Match 52.4%; Score 1064; DB 11; Length 1064;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1064; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 967 GGTGAGTAAACAGAACTTATTTTCCGGTTGAATTTGTTTAACTATTGAGATTGTGCTA 1026
DB 1 GGTGAGTAAACAGAACTTATTTTCCGGTTGAATTTGTTTAACTATTGAGATTGTGCTA 60
QY 1027 ACCGAAAAACAGAAACGGTTTATGACGCCAACGAGGCAAGGGGTAACAAACGAGAAAGGG 1086
DB 61 ACCGAAAAACAGAAACGGTTTATGACGCCAACGAGGCAAGGGGTAACAAACGAGAAAGGG 120
QY 1087 GATGGCGAAAAATCGTAAATTAACAGAAAAATAAGGGTGGTTTCACGATAAGTCTGCTA 1146
DB 121 GATGGCGAAAAATCGTAAATTAACAGAAAAATAAGGGTGGTTTCACGATAAGTCTGCTA 180
QY 1147 TATGACGCCAAAAAGGGTTCTTAAATTCAGAGAGACAATTAATCAGTTTTGTTGTTTGA 1206
DB 181 TATGACGCCAAAAAGGGTTCTTAAATTCAGAGAGACAATTAATCAGTTTTGTTGTTTGA 240
QY 1207 GAAGAAAGAAACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTTATCGTTTCAAGT 1266
DB 241 GAAGAAAGAAACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTTATCGTTTCAAGT 300
QY 1267 AGTCTCTTTATCAAACTCTTAAATTAACAAATCAAAACATGAAACACGTCGTCTTCG 1326
DB 301 AGTCTCTTTATCAAACTCTTAAATTAACAAATCAAAACATGAAACACGTCGTCTTCG 360
QY 1327 TTTTCGATTCTAGATACGATTTTTTTTCTCATGTGAATGAATCTGTTTTTATTACTACTAG 1386
DB 361 TTTTCGATTCTAGATACGATTTTTTTTCTCATGTGAATGAATCTGTTTTTATTACTACTAG 420
QY 1387 GGTGTTGTTCAATATTTTTCCGAGAAATTTACAGAGAGAAACAAAGTTAGTGATTTATGATGC 1446
DB 421 GGTGTTGTTCAATATTTTTCCGAGAAATTTACAGAGAGAAACAAAGTTAGTGATTTATGATGC 480
QY 1447 AGAGTATGAAGTAAATTTATATACATAAATCATGTTTTGTTCTCAAGCATCTACGTTGAAAT 1506
DB 481 AGAGTATGAAGTAAATTTATATACATAAATCATGTTTTGTTCTCAAGCATCTACGTTGAAAT 540
QY 1507 ATATATAAGAAAGTTTTTTTGGTGAAGAAATATGTATGAGAAAGTTTCATCTTTTCATAATA 1566
DB 541 ATATATAAGAAAGTTTTTTTGGTGAAGAAATATGTATGAGAAAGTTTCATCTTTTCATAATA 600
QY 1567 GTCAAAACAACTCTCTTTTCATACCAAAAAAATTTGAAAAAAATTTAGTGAACCTCTCT 1626
DB 601 GTCAAAACAACTCTCTTTTCATACCAAAAAAATTTGAAAAAAATTTAGTGAACCTCTCT 660
QY 1627 TTGTCGGATTAGTTAGTTAGTTGGACTCAGAAATCAAAATACGATTAGCATAAACAAATTTT 1686
DB 661 TTGTCGGATTAGTTAGTTAGTTGGACTCAGAAATCAAAATACGATTAGCATAAACAAATTTT 720
QY 1687 TGGCATGGCAATTTATGTCGACGTAAGTAATATACCAATAGAACATATTTTGGAGTA 1746
DB 721 TGGCATGGCAATTTATGTCGACGTAAGTAATATACCAATAGAACATATTTTGGAGTA 780
QY 1747 GTTAAGATTATGATTGAAGAAATACATTAACGATAAGCAATAAAATTTCTTTGCTGTTTC 1806
DB 781 GTTAAGATTATGATTGAAGAAATACATTAACGATAAGCAATAAAATTTCTTTGCTGTTTC 840
QY 1807 TTGGTTTTGTCGTTTTTATAGAAATGAAATATGTAATTTGTTTTTTTCCACAGTAGA 1866
DB 841 TTGGTTTTGTCGTTTTTATAGAAATGAAATATGTAATTTGTTTTTTTCCACAGTAGA 900
QY 1867 TATGTACTATACACATAAGTAACATGGTAGTTTATATAGAGAGAGATTGATTTTTTC 1926
DB 901 TATGTACTATACACATAAGTAACATGGTAGTTTATATAGAGAGAGATTGATTTTTTC 960
QY 1927 GTATATTTCTTTGTCGAAATAAATATGTAAGTAATTTATGTTTATTAATTTGACAGA 1986
DB 961 GTATATTTCTTTGTCGAAATAAATATGTAAGTAATTTATGTTTATTAATTTGACAGA 1020
QY 1987 TTTGTTCCAGTTGAGAAAGTTTAAATTTAGATTAAACACAAAAAG 2030
DB 1021 TTTGTTCCAGTTGAGAAAGTTTAAATTTAGATTAAACACAAAAAG 1064
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Db 1021 TTTGTTCCAGTCGAGAGTTTAATTAGATTAAACAACAAG 1064

RESULT 5

US-09-770-445-116/c  
; Sequence 116, Application US/09770445  
; Patent No. US20020023281A1

GENERAL INFORMATION:

; APPLICANT: Goriach, Jorn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.  
; APPLICANT: Price, Jennifer L.  
; APPLICANT: Raines, Tracy M.  
; APPLICANT: Yu, Yang  
; APPLICANT: Rameaka, Joshua G.  
; APPLICANT: Page, Amy  
; APPLICANT: Ledford, Brooke L.  
; APPLICANT: Woessner, Jeffrey P.  
; APPLICANT: Haas, William David  
; APPLICANT: Kricker, Ma'ja  
; APPLICANT: Slader, Ted  
; APPLICANT: Davis, Keith R.  
; APPLICANT: Allen, Keith  
; APPLICANT: Hoffman, Neil  
; APPLICANT: Hurban, Patrick  
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
; FILE REFERENCE: 2023US (PARA-012PRV)  
; CURRENT APPLICATION NUMBER: US/09/770,445  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/178,472  
; PRIOR FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 999  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 116  
; LENGTH: 1088  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-770-445-116

Query Match 2.6%; Score 53; DB 9; Length 1088;

Best Local Similarity 100.0%; Pred. No. 28-11; Mismatches 0; Indels 0; Gaps 0;

Matches 53; Conservative 0;

QY 1212 AGAAGAACAGATCAAAATACGAGAGAGATCTTAAAGAGATTTATCGTTTCAA 1264

DB 1066 AGNAGAACAGATCAAAATACGAGAGAGATCTTAAAGAGATTTATCGTTTCAA 1014

RESULT 6

US-10-424-599-140376/c  
; Sequence 140376, Application US/10424599  
; Publication No. US20040031072A1

GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 140376  
; LENGTH: 401  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_97769C.1  
US-10-424-599-140376

RESULT 8

US-09-925-065A-434756/c  
; Sequence 434756, Application US/09925065A  
; Publication No. US2005028172A9

GENERAL INFORMATION:

; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 434756  
; LENGTH: 558  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-434756

Query Match 1.2%; Score 24; DB 12; Length 558;

Best Local Similarity 100.0%; Pred. No. 4.2;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1.2%; Score 25; DB 18; Length 401;  
Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 AAAAGGAAAAAATAATATTTTT 102

DB 43 AAAGGAAAAAATAATATTTTT 19

RESULT 7

US-10-312-841-1  
; Sequence 1, Application US/10312841  
; Publication No. US20030186277A1

GENERAL INFORMATION:

; APPLICANT: Epigenomics AG  
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC  
; FILE REFERENCE: E01/1208/WO  
; CURRENT APPLICATION NUMBER: US/10/312,841  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 1  
; LENGTH: 3673778  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (3294164)  
US-10-312-841-1

Query Match 1.2%; Score 25; DB 16; Length 3673778;

Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1503 AAATATATATAAGAGTTTTTTTTT 1527

DB 1630300 AAATATATATAAGAGTTTTTTTTT 1630324

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QY 1592 AAAAAAAAAATTGAAAAAAAAATTAG 1615
DB 313 AAAAAAAAAATTGAAAAAAAAATTAG 290

RESULT 9
US-10-425-115-145853/c
; Sequence 145853, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 145853
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_64531C.1
US-10-425-115-145853

Query Match 1.1%; Score 23; DB 20; Length 250;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 AAGCAAAAAAAAAATAATTTTT 102
DB 108 AAGCAAAAAAAAAATAATTTTT 86

RESULT 10
US-10-108-260A-2360/c
; Sequence 2360, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2360
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-2360

Query Match 1.1%; Score 23; DB 17; Length 2550;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1928 TATATTTCTTTTGTGGAATAAA 1950
DB 1783 TATATTTCTTTTGTGGAATAAA 1761

RESULT 11
US-10-425-115-101814/c
; Sequence 101814, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

QY 1592 AAAAAAAAAATTGAAAAAAAAATTAG 1611
DB 149 AAAAAAAAAATTGAAAAAAAAATTAG 128

RESULT 12
US-10-357-930-60834/c
; Sequence 60834, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60834
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-60834

Query Match 1.1%; Score 22; DB 20; Length 468;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1590 AAAAAAAAAATTGAAAAAAAAAAA 1611
DB 149 AAAAAAAAAATTGAAAAAAAAAAA 128

RESULT 13
US-09-925-065A-297974
; Sequence 297974, Application US/09925065A
; Publication No. US20050228172A9
```

```
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 297974
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-297974
```

```
Query Match 1.1%; Score 22; DB 12; Length 574;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 ATTACAAAAGGAAAAAATAAT 94
Db 443 ATTACAAAAGGAAAAAATAAT 464
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## RESULT 14

```
US-09-925-065A-458650/c
; Sequence 458650, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 458650
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-458650
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Query Match 1.1%; Score 22; DB 12; Length 595;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1590 AAAAAAAAAATTGAAAAAAAAA 1611
Db 262 AAAAAAAAAATTGAAAAAAAAA 241
```

## RESULT 15

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US-09-925-065A-458651/c
; Sequence 458651, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 458651
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-458651
```

```
Query Match 1.1%; Score 22; DB 12; Length 595;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1590 AAAAAAAAAATTGAAAAAAAAA 1611
Db 262 AAAAAAAAAATTGAAAAAAAAA 241
```

Search completed: October 24, 2005, 06:44:08  
Job time : 2599 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 24, 2005, 00:50:38 ; Search time 6676 Seconds

(without alignments)  
11574.366 Million cell updates/sec

Title: US-10-643-676-1

Perfect score: 2030

Sequence: 1 cttcatagaagtgaccac.....ttagatttaaacacaaaaag 2030

Scoring table:

OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gest1:\*

9: gb\_gest2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	426	21.0	426	9	CC796106 SALK_0928
C 2	395	19.5	679	8	AQ961292 LERFK31TF
C 3	368	18.1	679	8	AQ961293 LERFK31TR
4	258	12.7	412	8	B2597205 SALK_1004
C 5	118	5.8	982	9	CL489509 SAIL_525
6	112	5.5	194	9	CF402809 Arabidops
7	103	5.1	246	8	BH809771 SALK_0056
C 8	95	4.7	396	9	CC796100 SALK_0927
9	88	4.3	207	1	AV832342 AV832342
10	88	4.3	278	1	AJ609323 AJ609323
11	86	4.3	507	1	AV825689 AV825689
C 12	86	4.2	605	5	BP562932 BP562932
13	84	4.1	463	7	T43139 T43139
14	84	4.1	495	7	H36351 H36351
15	83	4.1	516	7	BP561393 BP561393
16	79	3.9	636	5	CK119189 213m19.pl
17	78	3.8	515	7	CK119189 213m19.pl
18	78	3.8	894	7	CF652281 CF652281
19	74	3.6	314	7	T88394 T88394
20	74	3.6	569	7	T41663 T41663
21	67	3.3	349	7	T13967 T13967
22	67	3.3	400	7	T04382 T04382
23	66	3.3	362	7	N38594 N38594
24	66	3.3	422	7	R64904 R64904

R64851	13355	Lambd
H77166	17597	Lambd
H37321	15450	Lambd
T76560	11338	Lambd
T44522	7785	Lambd
T45972	9235	Lambd
H36812	14941	Lambd
CK119252	213101.pl	
R64820	13324	Lambd
R65167	13671	Lambd
N65161	20201	Lambd
T75683	10461	Lambd
T43969	7232	Lambd
T44460	7723	Lambd
T76049	10827	Lambd
N38557	19784	Lambd
T22553	4261	Lambd
CK117722	214h23.pl	
EX827666	Arabidops	
N96915	22290	Lambd
CB258391	30-E01108	
H76326	18031	Lambd
T43186	6449	Lambd
AV553768	AV553768	
T76917	11695	Lambd
H76463	18168	Lambd
CB262297	66-E8977-	
T42126	5389	Lambd
BZ355348	SALK_1266	
Z34671	ATT3431.Ve	
T46309	9572	Lambd
T43549	6812	Lambd
W43089	22470	Lambd
CB258452	06-E01108	
BP561200	BP561200	
BU636599	002A09.In	
BE038094	AA08G09.A	
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T45981	9244	Lambd
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T41751	10332	Lambd
T44572	7835	Lambd
T13996	2161	Lambd
BH439107	BOHAK61TR	
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BW550940	BW550940	
BW520746	BW520746	
BW561732	BW561732	
BW566410	BW566410	
A1686081	tw98f11.x	
A1627621	ty18h01.x	
A1465338	tj05c01.x	
BY696245	BY696245	
CC051946	CC051946	
BX783160	BX783160	
BH253111	SALK_0144	
CE633039	tigt-g88-	
BH745927	qz74a08.b	
CE931470	MBEGF16TR	
CK678882	2F101-F00	
CE231251	tigt-g88-	
BH994683	oeK41C03.	
B2062372	11e85b02.	
BH425590	BOGJF07TR	
AG480808	Mus muscu	
CK230311	ILLUMIGEN	
CR692849	Tetraodon	
AL803019	AL803019	
CR402810	Arabidops	
AA682395	z186c09.8	
BX746235	BX746235	
AU113083	AU113083	

98	23	1.1	300	1	AU115124	AU115124	171	23	1.1	1069	6	CD325027	CD325027	AGENCOURT
99	23	1.1	300	1	AU115813	AU115813	c 172	23	1.1	1425	9	AG320854	AG320854	Mus muscu
100	23	1.1	300	1	AU115864	AU115864	173	22	1.1	166	2	BE029931	BE029931	kp36908.y
101	23	1.1	300	1	AU116530	AU116530	c 174	22	1.1	185	9	CE538112	CE538112	tigr-g88-
102	23	1.1	300	6	C29544	C29544	175	22	1.1	191	6	CA341180	CA341180	haa80e05.
103	23	1.1	300	6	C32828	C32828	176	22	1.1	202	4	B1849732	B1849732	477657.MA
104	23	1.1	300	6	C57248	C57248	177	22	1.1	202	9	CL526039	CL526039	EY08717.D
105	23	1.1	300	6	C57422	C57422	178	22	1.1	225	5	BH844069	BH844069	AGENCOURT
106	23	1.1	300	6	C57691	C57691	179	22	1.1	227	5	BH960462	BH960462	AGENCOURT
107	23	1.1	344	1	AU211691	AU211691	180	22	1.1	230	4	B1746533	B1746533	rm28605.y
108	23	1.1	375	7	CR428049	CR428049	181	22	1.1	240	1	AU071654	AU071654	AU071654
109	23	1.1	425	8	BH173064	BH173064	182	22	1.1	240	1	AU072568	AU072568	AU072568
c 110	23	1.1	451	6	CB104242	CB104242	183	22	1.1	247	6	CA341165	CA341165	haa79912.
111	23	1.1	519	4	BJ815455	BJ815455	184	22	1.1	249	6	CA739149	CA739149	wpi28.pk0
112	23	1.1	534	1	BJ144876	BJ144876	c 185	22	1.1	254	7	CN751112	CN751112	ApHL3SD-I
113	23	1.1	547	4	AI065346	AI065346	186	22	1.1	277	1	AV529773	AV529773	AV529773
114	23	1.1	548	4	BJ780148	BJ780148	187	22	1.1	279	9	AL766416	AL766416	Arabi608
115	23	1.1	555	4	BJ787272	BJ787272	188	22	1.1	290	1	AV848388	AV848388	AV848388
c 116	23	1.1	555	7	CF403324	CF403324	189	22	1.1	318	2	BF605181	BF605181	271463.MA
117	23	1.1	566	7	CK553471	CK553471	c 190	22	1.1	324	5	BW009825	BW009825	BW009825
118	23	1.1	574	1	AL643196	AL643196	191	22	1.1	325	7	CK721101	CK721101	tad50n03.
119	23	1.1	575	4	BJ815759	BJ815759	192	22	1.1	329	2	AV997486	AV997486	AV997486
120	23	1.1	576	4	BJ784050	BJ784050	193	22	1.1	351	1	AA226320	AA226320	rc20c08.s
121	23	1.1	577	1	AL797114	AL797114	194	22	1.1	361	4	BG226617	BG226617	kp91e06.y
122	23	1.1	587	1	AL651939	AL651939	195	22	1.1	362	2	BE029053	BE029053	kd24c04.y
123	23	1.1	596	4	BJ375939	BJ375939	196	22	1.1	381	8	BZ477447	BZ477447	BONEG26TF
124	23	1.1	597	8	BH830615	BH830615	c 197	22	1.1	388	8	BH490847	BH490847	BOGIN73TR
125	23	1.1	606	7	CO122794	CO122794	198	22	1.1	402	2	AW963923	AW963923	EST375996
c 126	23	1.1	612	8	BZ509657	BZ509657	199	22	1.1	406	6	CA758925	CA758925	OE12B10.T
127	23	1.1	615	4	BJ783834	BJ783834	200	22	1.1	423	1	AU226827	AU226827	AU226827
128	23	1.1	616	4	BJ786358	BJ786358	201	22	1.1	424	6	CB475298	CB475298	jnb105.F0
c 129	23	1.1	616	6	CB534226	CB534226	202	22	1.1	425	4	BG019528	BG019528	daa21c04.
130	23	1.1	620	4	BJ776705	BJ776705	203	22	1.1	432	1	AU286777	AU286777	AU286777
c 131	23	1.1	627	7	CK947593	CK947593	204	22	1.1	457	2	AW235793	AW235793	xn22c12.x
132	23	1.1	629	4	BJ810742	BJ810742	c 205	22	1.1	468	6	BY701501	BY701501	BY701501
133	23	1.1	633	4	BJ792314	BJ792314	c 206	22	1.1	471	1	AI127091	AI127091	qb97g09.x
134	23	1.1	636	1	AL876013	AL876013	c 207	22	1.1	481	8	BH432980	BH432980	BOGLC85TF
135	23	1.1	636	4	BJ809769	BJ809769	208	22	1.1	485	7	CO132580	CO132580	GR_Eb451
c 136	23	1.1	642	4	BJ810694	BJ810694	209	22	1.1	494	2	BE223219	BE223219	kp74b04.y
c 137	23	1.1	647	1	AL870755	AL870755	c 210	22	1.1	496	9	CL873214	CL873214	abe87c07.
138	23	1.1	648	1	AL891461	AL891461	211	22	1.1	498	7	CO154891	CO154891	OB_Ba002
139	23	1.1	647	4	BJ815372	BJ815372	212	22	1.1	503	7	CO118559	CO118559	GR_Eb020
c 140	23	1.1	650	9	CE612712	CE612712	213	22	1.1	508	2	BE580949	BE580949	kp83e01.y
c 141	23	1.1	658	8	BH560797	BH560797	214	22	1.1	511	1	AU021880	AU021880	AU021880
c 142	23	1.1	662	6	CB535472	CB535472	215	22	1.1	516	7	CO082017	CO082017	GR_Ea46G
143	23	1.1	671	4	BJ797903	BJ797903	216	22	1.1	532	8	AZ128327	AZ128327	OSUNB309
c 144	23	1.1	680	6	CB468000	CB468000	217	22	1.1	533	2	AW496614	AW496614	kp03e10.y
c 145	23	1.1	685	6	CB438034	CB438034	c 218	22	1.1	541	8	AZ263258	AZ263258	RPCI-23-1
146	23	1.1	687	4	BJ782838	BJ782838	219	22	1.1	555	5	BP529839	BP529839	BP529839
147	23	1.1	695	1	AU213077	AU213077	220	22	1.1	560	7	CV465316	CV465316	taj26f10.
c 148	23	1.1	699	6	BY711080	BY711080	221	22	1.1	569	9	CC961362	CC961362	BOLEA44TR
c 149	23	1.1	705	9	CR824385	CR824385	222	22	1.1	578	7	CO073979	CO073979	GR_Ea33N
150	23	1.1	715	4	BJ794920	BJ794920	223	22	1.1	579	7	CO103660	CO103660	GR_Eb003
151	23	1.1	731	8	BH824376	BH824376	224	22	1.1	587	6	CA844825	CA844825	hab92b08.
152	23	1.1	738	2	BF678409	BF678409	225	22	1.1	604	5	BU495161	BU495161	PfESToab8
153	23	1.1	740	4	BJ154614	BJ154614	226	22	1.1	612	9	CNS040GW	CNS040GW	Tetraodon
154	23	1.1	756	7	CN168241	CN168241	c 227	22	1.1	613	9	CF657367	CF657367	tac74f11.
155	23	1.1	760	9	CS587124	CS587124	228	22	1.1	618	7	CF505946	CF505946	USDA-FP_1
156	23	1.1	767	7	CR580998	CR580998	229	22	1.1	623	9	CE470350	CE470350	tigr-g88-
157	23	1.1	777	5	BX698728	BX698728	230	22	1.1	627	8	BH559200	BH559200	BOGL38TR
c 158	23	1.1	786	7	CR564890	CR564890	231	22	1.1	631	8	BH685331	BH685331	BOMB49TR
159	23	1.1	798	5	BX718267	BX718267	232	22	1.1	649	8	AZ570242	AZ570242	272PvB06
160	23	1.1	800	8	BH477962	BH477962	233	22	1.1	651	8	BH987737	BH987737	oed09d04.
161	23	1.1	809	5	BX701238	BX701238	c 234	22	1.1	659	7	CN048526	CN048526	v2_p114_e
162	23	1.1	802	5	BX695380	BX695380	235	22	1.1	665	8	BH524284	BH524284	BOGCG40TR
163	23	1.1	813	8	BH558385	BH558385	236	22	1.1	670	8	AZ573465	AZ573465	317PvG01
c 164	23	1.1	832	8	AZ193186	AZ193186	237	22	1.1	672	8	BH521070	BH521070	BOGGM57TF
165	23	1.1	839	9	AG542833	AG542833	c 238	22	1.1	675	8	BZ179662	BZ179662	CH230-484
c 166	23	1.1	855	7	CK196558	CK196558	239	22	1.1	680	9	CE252481	CE252481	tigr-g88-
c 167	23	1.1	860	7	CR583704	CR583704	c 240	22	1.1	692	8	BH513027	BH513027	BOHKK08TR
168	23	1.1	861	8	BZ509941	BZ509941	241	22	1.1	696	8	AZ985740	AZ985740	2M027M11
169	23	1.1	1002	9	CL029400	CL029400	242	22	1.1	702	7	CF654199	CF654199	tac74f11.
170	23	1.1	1043	9	CL057311	CL057311	243	22	1.1	704	8	BZ036699	BZ036699	oeh35h11.

244	1.1	706	9	CE018520	tigr-g88-	317	21	1.0	298	7	CO942307	CO942307 UMC-P2mm1
245	22	733	6	AG537867	Mus muscu	C 318	21	1.0	301	1	AA598032	AA598032 29281 Lam
246	22	736	6	CB947571	AGENCOURT	319	21	1.0	320	5	BP604656	BP604656 BP604656
247	22	736	9	AG441391	Mus muscu	320	21	1.0	325	7	CR514555	CR514555 CR514555
248	22	755	6	CB953185	AGENCOURT	321	21	1.0	327	1	AI944701	AI944701 ba04d05.y
249	22	762	8	BZ048147	kg33a04.	322	21	1.0	334	7	T00052	T00052 *ESTT00773.Z
250	22	764	9	CE912524	t071020ba	323	21	1.0	341	4	BMI59706	BMI59706 EST562229
251	22	764	8	BZ428252	BONPCL17TR	324	21	1.0	345	7	BN018792	BN018792 ux80H09.x
252	22	770	8	AG537749	Mus muscu	325	21	1.0	364	2	BF018792	BF018792 602989710
253	22	774	9	CE820835	tigr-g88-	C 326	21	1.0	370	4	BI412493	BI412493 602989710
254	22	783	9	AG032294	Pan trogl	327	21	1.0	370	8	CL376469	CL376469 RPCI44.4
255	22	788	8	BH945848	obu91e09.	C 328	21	1.0	374	8	BL618961	BL618961 SALK_0400
256	22	791	8	BH588772	BOHLK81TH	329	21	1.0	377	6	CAB19562	CAB19562 sau80611.
257	22	797	8	CG339917	QOAK81TH	330	21	1.0	386	1	AL790677	AL790677 AL790677
258	22	805	9	CG678715	ZMMBB029	331	21	1.0	387	8	B31605	B31605 HS-1011-A2-
259	22	817	9	CR307559	Medicago	332	21	1.0	389	7	CO098817	CO098817 GR_Ea23F
260	22	820	8	BZ482438	BONLS89TR	C 333	21	1.0	397	6	BY701502	BY701502 BV701502
261	22	828	8	BH441162	BOGQL32TR	334	21	1.0	405	5	BP658043	BP658043 BP658043
262	22	834	5	BH421180	AGENCOURT	335	21	1.0	410	9	EX656137	EX656137 Arabidops
263	22	838	8	BZ478437	BONHR80TF	336	21	1.0	411	1	AU287295	AU287295 AU287295
264	22	838	8	BH657873	BOHUR09TR	337	21	1.0	415	2	BF406978	BF406978 UI-R-BJ2-
265	22	852	9	AG472015	Mus muscu	C 338	21	1.0	415	4	BM161558	BM161558 EST564081
266	22	854	7	CK161044	FGAS04271	C 339	21	1.0	422	8	BH117579	BH117579 RPCI-24-2
267	22	863	7	BF785633	AGENCOURT	340	21	1.0	424	4	BI276797	BI276797 UI-R-CX0-
268	22	867	4	CG309901	HVSMC001	341	21	1.0	424	8	BH248417	BH248417 BOAG26TF
269	22	886	8	BZ434167	BONRD80TR	C 342	21	1.0	425	5	EX689801	EX689801 BX689801
270	22	890	9	CL067679	Medicago	C 343	21	1.0	427	2	AW084190	AW084190 xc48H03.x
271	22	891	9	CR318708	Medicago	C 344	21	1.0	433	5	BU757580	BU757580 UI-1-CF0-
272	22	892	4	BM358164	Ea000	C 345	21	1.0	434	5	RG365016	RG365016 104797 MA
273	22	895	9	CG960097	MBEHE73TR	C 346	21	1.0	438	5	BQ892044	BQ892044 AGENCOURT
274	22	896	2	BE053710	GA_Ea003	C 347	21	1.0	447	5	BI083273	BI083273 602875192
275	22	904	9	CL481284	SATL_339	348	21	1.0	447	5	BQ031485	BQ031485 UI-1-CF0-
276	22	905	8	CC339924	OQAK81TV	C 349	21	1.0	450	2	BF401454	BF401454 UI-R-CA0-
277	22	906	7	CR418027	CR418027	C 350	21	1.0	451	9	CE532700	CE532700 tigr-g88-
278	22	912	5	BU912884	AGENCOURT	C 351	21	1.0	454	1	AI475283	AI475283 t181c03.x
279	22	928	9	CL070690	CH216-119	C 352	21	1.0	454	5	BP587449	BP587449 BP587449
280	22	929	9	CL071159	CH216-120	353	21	1.0	464	9	CL874742	CL874742 abe98c10.
281	22	969	9	CG768497	TcB47.2_A	C 354	21	1.0	469	7	T93843	T93843 ye05f03.r1
282	22	997	9	CNS07CS2	T3_end	C 355	21	1.0	489	8	BZ507738	BZ507738 BONNH55TR
283	22	998	9	CL066158	CH216-108	C 356	21	1.0	491	7	CO647252	CO647252 ILLUMIGEN
284	22	999	6	CD051186	AGENCOURT	C 357	21	1.0	491	8	CC459833	CC459833 SALK_1336
285	22	1005	4	BM801032	AGENCOURT	C 358	21	1.0	510	6	CB782711	CB782711 AMGNNUC:N
286	22	1019	8	CC268975	CH261-60D	359	21	1.0	513	1	AI716524	AI716524 UI-R-Y0-a
287	22	1043	9	CNS06C91	T7_end	C 360	21	1.0	516	5	BQ207626	BQ207626 UI-R-DY1-
288	22	1135	9	CL027221	CH216-25G	C 361	21	1.0	523	9	CL773698	CL773698 OR_BBA008
289	22	1190	3	AG346314	Mus muscu	C 362	21	1.0	529	6	BY593199	BY593199 BY593199
290	22	1196	9	AG346314	Mus muscu	C 363	21	1.0	531	1	AI442890	AI442890 sa28c03.x
291	22	1197	3	CR679028	Tetraodon	C 364	21	1.0	534	5	EX836397	EX836397 BX836397
292	22	1203	8	CC275232	CH261-931	C 365	21	1.0	538	8	AO611353	AO611353 HS_5088B
293	22	1247	9	CG756067	P051-2-G0	C 366	21	1.0	539	1	AL914006	AL914006 AG-ND-169
294	22	1300	9	CG754066	CH216-170	C 367	21	1.0	544	8	BH399346	BH399346 AG-ND-169
295	22	1370	8	CC214165	CH261-177	C 368	21	1.0	548	9	CR348902	CR348902 Medicago
296	22	1402	9	CG750735	P045-2-B0	C 369	21	1.0	551	8	CC460022	CC460022 SALK_1384
297	22	1586	3	CR679862	Tetraodon	C 370	21	1.0	556	8	AZ424325	AZ424325 IM0203F22
298	22	109	7	CNS63166	CH216-170	C 371	21	1.0	556	8	AZ424325	AZ424325 IM0203F22
299	21	131	9	CR395843	Arabidops	C 372	21	1.0	561	4	BI804888	BI804888 S001F08.S
300	21	131	9	CR395843	Arabidops	C 373	21	1.0	561	8	AO780691	AO780691 HS_3169.A
301	21	154	7	CK372788	la191901.	374	21	1.0	565	8	BH884121	BH884121 hw49h02.g
302	21	182	7	CO819074	CSECS124B	375	21	1.0	571	8	BZ302233	BZ302233 KD1724.pl
303	21	206	9	CE589497	tigr-g88-	376	21	1.0	587	8	B62592	B62592 T22G15TR.TA
304	21	214	5	BQ352247	RCO-HT077	377	21	1.0	589	1	AU288091	AU288091 AU288091
305	21	218	4	BM161736	EST564259	C 378	21	1.0	593	5	BU897943	BU897943 X072C12.P
306	21	218	4	BM162558	EST564259	C 379	21	1.0	605	7	CF372166	CF372166 CSECS049B
307	21	218	4	BM170990	EST573513	C 380	21	1.0	605	9	BX968527	BX968527 Forward.B
308	21	238	4	BM169266	EST571789	C 381	21	1.0	608	8	BH769531	BH769531 BMAC366D
309	21	238	9	CC607455	OQOBR90TH	C 382	21	1.0	616	9	AG589467	AG589467 Mus muscu
310	21	242	4	BM166537	EST569060	383	21	1.0	616	9	BI066757	BI066757 pgfin.pk0
311	21	256	4	BM168436	EST570959	384	21	1.0	617	2	AG589467	AG589467 Mus muscu
312	21	274	1	AV139759	AV139759	385	21	1.0	617	9	CE351375	CE351375 tigr-g88-
313	21	274	2	BF343057	BF343057	386	21	1.0	630	7	CO083635	CO083635 GR_Ea48M
314	21	283	2	BF148282	uy84h03.x	C 387	21	1.0	630	7	CL807946	CL807946 OR_CBA002
315	21	291	1	AI412123	EST240417	388	21	1.0	635	2	BE821946	BE821946 GM700016A
316	21	297	9	CC883632	SALK_0953	389	21	1.0	635	2	BE821946	BE821946 GM700016A

390	21	1.0	640	8	BH579760	BOG5Y68TR	C 463	21	1.0	825	8	BZ466087	BOHQD911T
391	21	1.0	645	6	CB367065	O2322 oOk	C 464	21	1.0	825	9	CL133100	ISB1-103A
C 392	21	1.0	646	8	AZ522836	211PB609	C 465	21	1.0	826	9	BH154380	ENTRS55TF
393	21	1.0	647	2	BB620417	BB620417	C 466	21	1.0	828	9	CL848359	OR_CBA007
394	21	1.0	651	8	BZ497631	BONMQ81TF	C 467	21	1.0	833	9	CC635333	OGUHB26TM
C 395	21	1.0	659	8	BZ010647	oeH81d07.	C 468	21	1.0	833	9	CL794632	OR_CBA000
C 396	21	1.0	662	3	CR694175	Tetraodon	C 469	21	1.0	834	8	AZ196304	SP_1031_B
C 397	21	1.0	664	5	BP020703	BP020703	C 470	21	1.0	844	9	CL133517	ISB1-103K
C 398	21	1.0	666	1	AL716319	AL716319	C 471	21	1.0	851	8	CG366345	PUMH807TB
C 399	21	1.0	670	7	CF237993	CF237993	C 472	21	1.0	851	8	CG303853	OG1CY47TH
C 400	21	1.0	673	2	BB650922	BB650922	C 473	21	1.0	853	5	BU957112	AGENCOURT
C 401	21	1.0	674	8	AZ571175	283PVG12	C 474	21	1.0	859	7	CR438365	CR438365
C 402	21	1.0	676	5	BQ211409	UI-R-DY1-	C 475	21	1.0	865	9	CG337653	CG337653
403	21	1.0	678	5	BO193567	UI-R-DK1-	C 476	21	1.0	866	5	BU251815	AGENCOURT
404	21	1.0	678	6	CA508216	UI-R-FS0-	C 477	21	1.0	871	6	CD251683	AGENCOURT
C 405	21	1.0	681	8	BH975208	odh65e09.	C 478	21	1.0	874	2	BF685099	AGENCOURT
406	21	1.0	682	9	CE831405	tigr-9ss-	C 479	21	1.0	876	6	CB589348	AGENCOURT
407	21	1.0	684	1	AL716264	AL716264	C 480	21	1.0	883	8	AZ184957	SP_1003_B
C 408	21	1.0	685	9	CG308284	OGVDC90TV	C 481	21	1.0	883	9	CC487609	CH240_319
C 409	21	1.0	686	1	AV682222	AV682222	C 482	21	1.0	905	8	AQ747078	HS_5538_A
C 410	21	1.0	689	6	CB200534	AGENCOURT	C 483	21	1.0	906	7	BF682145	AGENCOURT
411	21	1.0	691	9	CL630099	CL630099	C 484	21	1.0	910	5	BO962145	AGENCOURT
412	21	1.0	692	8	BZ000066	oe103f05.	C 485	21	1.0	910	9	AG474136	Mus muscu
C 413	21	1.0	693	8	BZ032411	oeF99e09.	C 486	21	1.0	911	9	CG953956	MBEG102TF
C 414	21	1.0	693	8	BZ488794	BONDB86TF	C 487	21	1.0	912	8	BH134673	ENTOM66TR
415	21	1.0	694	9	CL823468	OR_CBA004	C 488	21	1.0	913	5	BU561890	AGENCOURT
416	21	1.0	697	8	BH442176	BOQPD52TF	C 489	21	1.0	917	8	CC090976	CSU_K33r.
C 417	21	1.0	697	8	BZ004758	oecl7h06.	C 490	21	1.0	919	8	AZ547419	AGENCOURT
418	21	1.0	698	5	BQ203268	UI-R-DN1-	C 491	21	1.0	923	7	CO023893	ESU789026
419	21	1.0	702	4	BM391454	UI-R-DY0-	C 492	21	1.0	924	6	CD387609	AGENCOURT
C 420	21	1.0	703	8	BH997905	oeq87h04.	C 493	21	1.0	931	9	CL483650	SAIL_384
421	21	1.0	704	8	BZ009759	oeH97c07.	C 494	21	1.0	949	9	CL044206	AGENCOURT
C 422	21	1.0	705	9	CE602884	CS603884	C 495	21	1.0	956	7	CFN806572	ILLUMIGEN
C 423	21	1.0	707	5	BW387718	BW387718	C 496	21	1.0	965	7	CF224719	AGENCOURT
424	21	1.0	710	7	CN980259	31600_125	C 497	21	1.0	969	5	BU153272	Tetraodon
425	21	1.0	712	5	AG478266	Mus muscu	C 498	21	1.0	969	8	BF157931	ENTRX25TF
C 426	21	1.0	713	9	BQ192949	UI-R-DK1-	C 499	21	1.0	975	5	CN2401UGS	Tetraodon
427	21	1.0	714	9	CL818786	CL818786	C 500	21	1.0	975	5	BQ224807	AGENCOURT
C 428	21	1.0	715	9	CL858428	OR_CBA008	C 501	21	1.0	976	5	BQ224807	AGENCOURT
C 429	21	1.0	716	8	BH995966	BH995966	C 502	21	1.0	984	9	CL088471	ISB1-11A5
430	21	1.0	719	9	CL754822	CL754822	C 503	21	1.0	989	6	CD244235	AGENCOURT
431	21	1.0	728	9	CL807901	CL807901	C 504	21	1.0	992	2	BE052563	GA_Ea003
432	21	1.0	729	9	CL621467	OR_BBA001	C 505	21	1.0	995	9	AG421360	Mus muscu
433	21	1.0	730	5	BQ200347	UI-R-D21-	C 506	21	1.0	1002	7	CN802082	ILLUMIGEN
C 434	21	1.0	741	9	CL563819	OB_Ba002	C 507	21	1.0	1005	6	CA981206	AGENCOURT
C 435	21	1.0	751	9	AG459061	Mus muscu	C 508	21	1.0	1011	3	CA981206	AGENCOURT
C 436	21	1.0	755	7	CF784870	CF784870	C 509	21	1.0	1015	5	BU147972	Tetraodon
C 437	21	1.0	759	8	AQ328757	nbxb0043F	C 510	21	1.0	1022	6	CD390247	AGENCOURT
438	21	1.0	760	7	CN323267	AGENCOURT	C 511	21	1.0	1032	9	CL078498	CH216-150
439	21	1.0	761	8	AZ548469	AZ548469	C 512	21	1.0	1036	5	BE964148	601657832
440	21	1.0	762	9	CL826664	OR_CBA004	C 513	21	1.0	1044	5	BQ214032	AGENCOURT
441	21	1.0	764	4	BG784651	SEAMUC004	C 514	21	1.0	1053	6	CD107800	AGENCOURT
442	21	1.0	772	8	BH710780	BOHTL20TF	C 515	21	1.0	1062	8	BZ694141	SP_Ba004
443	21	1.0	772	8	BH710780	Mus muscu	C 516	21	1.0	1076	9	AG341839	Mus muscu
444	21	1.0	776	9	AG464991	AG464991	C 517	21	1.0	1079	5	BM927085	AGENCOURT
445	21	1.0	780	8	AQ330270	nbxb0046H	C 518	21	1.0	1092	4	BM800110	AGENCOURT
446	21	1.0	785	9	AG530474	Mus muscu	C 519	21	1.0	1094	9	CL059582	CH216-90E
447	21	1.0	788	8	BH521150	BOHKO46TR	C 520	21	1.0	1097	8	CL081948	CH216-164
448	21	1.0	790	6	CB203314	AGENCOURT	C 521	21	1.0	1104	7	CK211752	CH216-9A1
C 449	21	1.0	790	6	CL711027	OR_BBA003	C 522	21	1.0	1114	8	CK211752	FGAS02360
C 450	21	1.0	795	8	BH478652	BOHMK48TF	C 523	21	1.0	1117	7	CL048051	CH216-67E
451	21	1.0	798	9	AG416918	Mus muscu	C 524	21	1.0	1124	9	CL062553	CH216-110
C 452	21	1.0	799	4	BG917288	BG917288	C 525	21	1.0	1130	9	CL04051	CH216-164
453	21	1.0	799	9	BX151844	Danio rer	C 526	21	1.0	1158	8	CC194442	CH216-9A1
C 454	21	1.0	800	4	BG783688	SEAMUC003	C 527	21	1.0	1158	8	CC264393	CH216-67E
C 455	21	1.0	802	9	AG177437	Pan trogl	C 528	21	1.0	1180	7	CO384348	CH216-98F
456	21	1.0	804	8	AG388461	Mus muscu	C 529	21	1.0	1196	4	BM466675	CH261-110
C 457	21	1.0	804	8	BH965599	oddb7e11.	C 530	21	1.0	1200	3	CK221115	CH261-42J
458	21	1.0	807	9	CR173578	Reverse 8	C 531	21	1.0	1205	3	CF676531	Tetraodon
C 459	21	1.0	812	9	CG337645	OGWIR16TH	C 532	21	1.0	1205	3	CF676531	Tetraodon
460	21	1.0	814	6	CA465152	CA465152	C 533	21	1.0	1212	3	CR665685	Tetraodon
C 461	21	1.0	818	8	BZ392036	EINBJ49TF	C 534	21	1.0	1216	3	CG750871	P045-2-E1
C 462	21	1.0	822	9	CL764888	OR_BBA013	C 535	21	1.0	1223	8	CC268294	CH261-149



C 536	1.0	1273	9	CL021453	CL021453	CH216-8G1	C 609	20	1.0	340	7	T89114	T89114	yc84hl2.e1
C 537	1.0	1280	9	CL080475	CL080475	CH216-158	C 610	20	1.0	343	2	BF392658	BF392658	UI-R-CA0-
C 538	1.0	1296	4	BM467347	BM467347	AGENCOURT	C 611	20	1.0	346	7	CK746829	CK746829	asm01-8mb
C 539	1.0	1307	8	CC238331	CC238331	CH261-192	C 612	20	1.0	353	7	CR585105	CR585105	CR585105
C 540	1.0	1378	9	CG744810	CG744810	P037-3-B0	C 613	20	1.0	358	4	BM093512	BM093512	8s109g11.
C 541	1.0	1467	9	AG276258	AG276258	Mus muscu	C 614	20	1.0	362	5	BQ265755	BQ265755	NISC-ff08
C 542	1.0	2348	3	AK082373	AK082373	Mus muscu	C 615	20	1.0	369	2	BE046033	BE046033	hd91h03.x
C 543	1.0	2927	3	AK035855	AK035855	Mus muscu	C 616	20	1.0	372	4	BG626208	BG626208	CC-eafic1c
C 544	1.0	69	9	CR396216	CR396216	Arabidops	C 617	20	1.0	372	9	AG199023	AG199023	Pan trogl
C 545	1.0	109	7	CV286121	CV286121	tak66a03.	C 618	20	1.0	374	4	BI494148	BI494148	df10Ba08.
C 546	1.0	121	9	BX663279	BX663279	Arabidops	C 619	20	1.0	374	7	CR585106	CR585106	CR585106
C 547	1.0	137	9	CR271484	CR271484	Forward s	C 620	20	1.0	376	8	AQ031215	AQ031215	HS 2214.A
C 548	1.0	142	9	CR402516	CR402516	Arabidops	C 621	20	1.0	378	4	BQ027317	BQ027317	602296031
C 549	1.0	150	9	CG479459	CG479459	OST10324	C 622	20	1.0	382	6	CB477376	CB477376	jnb20.G07
C 550	1.0	154	1	AL898443	AL898443	AL898443	C 623	20	1.0	383	1	AI711079	AI711079	UI-R-AE1-
C 551	1.0	154	1	AU197517	AU197517	AU197517	C 624	20	1.0	384	5	BP506991	BP506991	P00
C 552	1.0	155	9	BX652345	BX652345	Arabidops	C 625	20	1.0	385	5	BP506991	BP506991	BP506991
C 553	1.0	155	9	BX652345	BX652345	Arabidops	C 626	20	1.0	385	8	BZ942645	BZ942645	CH240.93P
C 554	1.0	180	8	AZ023673	AZ023673	RFC1-23-3	C 627	20	1.0	387	6	CD447293	CD447293	E0492707
C 555	1.0	185	9	AG021707	AG021707	Oryza sat	C 628	20	1.0	388	1	AL387115	AL387115	MCBCA0E05
C 556	1.0	193	4	BG237554	BG237554	bab14b03.	C 629	20	1.0	388	1	AA563094	AA563094	vk52d10.f
C 557	1.0	197	7	H74980	H74980	568 Random-	C 630	20	1.0	388	8	AZ513003	AZ513003	1M0358K23
C 558	1.0	199	8	BH619074	BH619074	SALK_0402	C 631	20	1.0	388	8	BZ176141	BZ176141	CH230-397
C 559	1.0	201	6	CB818268	CB818268	sal123pz.f	C 632	20	1.0	389	1	AI968124	AI968124	wul3d07.x
C 560	1.0	205	4	BI743670	BI743670	kx50d01.y	C 633	20	1.0	391	1	AV816635	AV816635	AV816635
C 561	1.0	207	9	CR402515	CR402515	Arabidops	C 634	20	1.0	391	4	BI183288	BI183288	UNL-P-FN-
C 562	1.0	212	4	EJ051349	EJ051349	EJ051349	C 635	20	1.0	393	1	AI603431	AI603431	UI-R-AC1-
C 563	1.0	216	2	BF223998	BF223998	BF223998	C 636	20	1.0	398	1	AA576018	AA576018	nm57d05.8
C 564	1.0	216	2	BE672366	BE672366	7a56f06.x	C 637	20	1.0	401	5	BQ297712	BQ297712	8ac01f04.
C 565	1.0	220	9	CE496100	CE496100	tigr-gss-	C 638	20	1.0	401	6	CA150676	CA150676	SCBFR2204
C 566	1.0	221	2	AW196585	AW196585	xm35b01.x	C 639	20	1.0	402	1	AU182665	AU182665	AU182665
C 567	1.0	223	5	AL771927	AL771927	Arabidops	C 640	20	1.0	404	8	BZ696711	BZ696711	SP_0051.B
C 568	1.0	224	5	BQ834098	BQ834098	Arabidops	C 641	20	1.0	404	8	AQ494596	AQ494596	HS_5171.B
C 569	1.0	224	9	CE397193	CE397193	tigr-gss-	C 642	20	1.0	406	1	AI869663	AI869663	nm02b01.x
C 570	1.0	226	9	CE397193	CE397193	Danio rer	C 643	20	1.0	411	2	BE603878	BE603878	BE603878
C 571	1.0	228	9	CR43E14S	CR43E14S	C99469	C 644	20	1.0	414	6	BY666701	BY666701	BY666701
C 572	1.0	229	6	D99469	D99469	C99469	C 645	20	1.0	416	2	BF407098	BF407098	UI-R-BJ2-
C 573	1.0	229	6	CK088013	CK088013	A031P27.3	C 646	20	1.0	417	1	AI023086	AI023086	OW53a03.8
C 574	1.0	248	7	CNS76214	CNS76214	rc25g12.x	C 647	20	1.0	417	7	CV296543	CV296543	EST884920
C 575	1.0	249	7	CNS75099	CNS75099	010131AAR	C 648	20	1.0	417	7	CV296543	CV296543	EST884920
C 576	1.0	251	1	AV377096	AV377096	AV377096	C 649	20	1.0	418	4	BI745271	BI745271	rx98d02.y
C 577	1.0	251	1	AI717221	AI717221	UI-R-Y0-a	C 650	20	1.0	418	4	BI745271	BI745271	rx98d02.y
C 578	1.0	256	2	AW312154	AW312154	6438 MARC	C 651	20	1.0	419	1	AI142921	AI142921	OZ45d08.x
C 579	1.0	256	2	AW312155	AW312155	6439 MARC	C 652	20	1.0	419	2	BE103078	BE103078	UI-R-BX0-
C 580	1.0	256	2	BE941680	BE941680	EST421259	C 653	20	1.0	419	8	AZ657284	AZ657284	1M0533E24
C 581	1.0	256	6	CB476876	CB476876	jnb13_B07	C 654	20	1.0	421	1	AI637665	AI637665	tt10908.x
C 582	1.0	256	6	AL771928	AL771928	Arabidops	C 655	20	1.0	421	4	BM285549	BM285549	UI-R-DK0-
C 583	1.0	262	2	BE063882	BE063882	QV3-BT029	C 656	20	1.0	421	4	BH239686	BH239686	AT1CD90TR
C 584	1.0	262	8	AZ617225	AZ617225	1M0448H23	C 657	20	1.0	424	5	BQ451056	BQ451056	PFEST0ab0
C 585	1.0	269	4	BJ329492	BJ329492	BJ329492	C 658	20	1.0	424	5	BH239686	BH239686	PFEST0ab0
C 586	1.0	270	2	BB116721	BB116721	BB116721	C 659	20	1.0	424	8	AQ353154	AQ353154	CITB1-E1-
C 587	1.0	276	1	AL387116	AL387116	MCBCA0E05	C 660	20	1.0	426	5	BP636662	BP636662	BP636662
C 588	1.0	279	1	AA841756	AA841756	MB3D6V6H0	C 661	20	1.0	426	5	BP636662	BP636662	BP636662
C 589	1.0	280	2	AW535862	AW535862	UI-R-B50-	C 662	20	1.0	427	1	AI038850	AI038850	ox48g01.x
C 590	1.0	286	1	AV228951	AV228951	AV228951	C 663	20	1.0	429	7	CV266036	CV266036	WS02028.B
C 591	1.0	290	1	AV286330	AV286330	AV286330	C 664	20	1.0	429	8	CC051276	CC051276	SALK_0042
C 592	1.0	292	5	B0497621	B0497621	PFEST0ab8	C 665	20	1.0	430	7	CN777518	CN777518	taf64g04.
C 593	1.0	292	7	CR473140	CR473140	CR473140	C 666	20	1.0	430	9	CE094776	CE094776	tigr-gss-
C 594	1.0	293	4	BI276358	BI276358	UI-R-CW0-	C 667	20	1.0	430	9	CE094776	CE094776	tigr-gss-
C 595	1.0	293	5	BM958593	BM958593	PLATE_6_E	C 668	20	1.0	431	1	AA976171	AA976171	on33e03.8
C 596	1.0	294	9	CL655629	CL655629	PR10124a	C 669	20	1.0	435	2	BB357604	BB357604	BR357604
C 597	1.0	296	8	AQ892801	AQ892801	HS_3156.B	C 670	20	1.0	435	6	BY697059	BY697059	BY697059
C 598	1.0	299	8	B2822871	B2822871	PUFHUI3TD	C 671	20	1.0	436	4	BI450200	BI450200	da676c11.
C 599	1.0	308	1	AI071417	AI071417	UI-R-C2-n	C 672	20	1.0	437	1	AV548729	AV548729	AV548729
C 600	1.0	308	1	AI307315	AI307315	tb18h02.x	C 673	20	1.0	438	8	AQ842304	AQ842304	fw62h10.x
C 601	1.0	315	7	CN777266	CN777266	taf64g04.	C 674	20	1.0	438	4	BM264824	BM264824	tw62h10.x
C 602	1.0	316	1	AV340139	AV340139	AV340139	C 675	20	1.0	438	8	AZ438702	AZ438702	1M0228J21
C 603	1.0	320	6	CA998835	CA998835	S234J_G12	C 676	20	1.0	439	2	BF394433	BF394433	IM0228J21
C 604	1.0	328	1	AL718854	AL718854	AL718854	C 677	20	1.0	442	1	AJ555592	AJ555592	UI-R-CA0-
C 605	1.0	335	1	AL718792	AL718792	AL718792	C 678	20	1.0	442	1	CB967127	CB967127	CB967127
C 606	1.0	337	7	CF226888	CF226888	EST1891.T	C 679	20	1.0	446	6	AL970529	AL970529	AL970529
C 607	1.0	339	6	CA761783	CA761783	BR060013A	C 680	20	1.0	446	5	BM517688	BM517688	BM517688
C 608	1.0	340	6	BY589623	BY589623	BY589623	C 681	20	1.0	448	2	AU094162	AU094162	AU094162
										449	2	AW469597	AW469597	hd29h06.x

682	20	1.0	450	2	BE603983	BE603983 GS323-T7	755	20	1.0	514	1	AA646426	AA646426 v832q12.r
683	20	1.0	450	4	BM089881	BM089881 503743 MA	c 756	20	1.0	514	1	AA890379	AA890379 ak13501.s
c 684	20	1.0	450	8	AZ614923	AZ614923 IM0443P24	c 757	20	1.0	516	1	AI071451	AI071451 UI-R-C1-k
685	20	1.0	451	5	BUS32846	BUS32846 AGENCOURT	c 758	20	1.0	518	5	BX518489	BX518489 BX518489
c 686	20	1.0	453	8	AZ147446	AZ147446 SP 0051.B	c 759	20	1.0	520	6	CD286777	CD286777 13_H4.abd
c 687	20	1.0	453	8	AZ766006	AZ766006 IM0563G15	c 760	20	1.0	520	8	BZ645682	BZ645682 OGANK15TM
688	20	1.0	455	1	AI607657	AI607657 vK52d10.y	c 761	20	1.0	522	4	BG374337	BG374337 UI-R-CV1-
c 689	20	1.0	455	7	CO106500	CO106500 GR_EB003	c 762	20	1.0	522	4	BJ087840	BJ087840 BJ087840
c 690	20	1.0	456	7	RA1674	RA1674 yf96c10.s1	c 763	20	1.0	522	4	CF331346	CF331346 NACL--07-
691	20	1.0	458	6	BY590498	BY590498 BY590498	c 764	20	1.0	523	8	AQ216493	AQ216493 HS_3241.B
692	20	1.0	458	7	CO110361	CO110361 GR_EB004	c 765	20	1.0	528	1	AU238852	AU238852 AU238852
693	20	1.0	458	7	CO131930	CO131930 GR_EB44H	c 766	20	1.0	528	8	AO423245	AO423245 CITBI-E1-
c 694	20	1.0	461	1	AI803878	AI803878 tp30e11.x	c 767	20	1.0	529	5	BU873155	BU873155 QO51G08.P
c 695	20	1.0	461	2	BF514567	BF514567 UI-H-BW1-	c 768	20	1.0	529	6	CD812889	CD812889 EN10_0220
c 696	20	1.0	462	1	AI263871	AI263871 q108C02.x	c 769	20	1.0	529	7	CO093655	CO093655 GR_Ea15F
697	20	1.0	463	7	CF536105	CF536105 UI-M-G10-	c 770	20	1.0	530	3	AK020140	AK020140 Mus_muscu
c 698	20	1.0	464	5	BX074618	BX074618 BX074618	771	20	1.0	532	5	BX719469	BX719469 BX719469
c 699	20	1.0	465	4	B1183996	B1183996 UNL-P-FN-	772	20	1.0	533	9	CL605701	CL605701 CH240_183
c 700	20	1.0	465	8	BH740202	BH740202 gf27a06.b	c 773	20	1.0	534	1	AL673936	AL673936 AL673936
701	20	1.0	465	8	BZ645673	BZ645673 OGANK15TC	c 774	20	1.0	535	1	AL899290	AL899290 AL899290
c 702	20	1.0	466	1	AI263875	AI263875 q108C08.x	c 775	20	1.0	539	1	AJ914099	AJ914099 AJ914099
c 703	20	1.0	466	2	AW099311	AW099311 g38B08.y	c 776	20	1.0	539	1	AV591376	AV591376 AV591376
704	20	1.0	466	5	BM958962	BM958962 PLATE 17	c 777	20	1.0	542	2	BE567770	BE567770 601340436
705	20	1.0	467	6	CD843533	CD843533 RPO2_1323	c 778	20	1.0	542	7	CF361485	CF361485 827818.MA
c 706	20	1.0	469	2	AW099320	AW099320 g38C08.y	c 779	20	1.0	543	5	BX094920	BX094920 BX094920
c 707	20	1.0	470	6	BY592340	BY592340 BY592340	c 780	20	1.0	543	6	BX719389	BX719389 BX719389
c 708	20	1.0	471	8	BZ498830	BZ498830 BONOQ56TR	781	20	1.0	545	2	AW979392	AW979392 EST310450
c 709	20	1.0	472	1	AL382713	AL382713 MLCBC09E08	782	20	1.0	547	9	AG253109	AG253109 Lotus cor
c 710	20	1.0	472	6	CD099530	CD099530 AGENCOURT	783	20	1.0	550	2	AW937930	AW937930 QVO-DT004
c 711	20	1.0	472	7	R60731	R60731 yho2d12.s1	784	20	1.0	551	7	CF258587	CF258587 A382.ab1
c 712	20	1.0	473	9	CC793951	CC793951 SALK_0390	c 785	20	1.0	552	9	CE334517	CE334517 tigr-g88-
c 713	20	1.0	474	2	BE996388	BE996388 UI-M-CG0p	c 786	20	1.0	554	9	CE943392	CE943392 BOIB088TR
c 714	20	1.0	474	5	BX073418	BX073418 BX073418	787	20	1.0	555	5	BU544970	BU544970 GM880005B
c 715	20	1.0	476	2	BE570498	BE570498 601328611	788	20	1.0	557	5	BX686902	BX686902 BX686902
c 716	20	1.0	476	5	BM958982	BM958982 PLATE 12	789	20	1.0	557	7	W56136	W56136 zc58b05.r1
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c 718	20	1.0	476	9	CR311246	CR311246 Medicago	c 791	20	1.0	560	6	CA302655	CA302655 taa14h05.
c 719	20	1.0	477	6	CB491154	CB491154 cmykrtCHO	c 792	20	1.0	560	7	CO584415	CO584415 DG2-10356
c 720	20	1.0	478	2	AW085982	AW085982 xc76e04.x	793	20	1.0	560	9	CR136705	CR136705 Reverse s
721	20	1.0	479	5	BP051907	BP051907 BP051907	c 794	20	1.0	561	5	BX684839	BX684839 BX684839
c 722	20	1.0	479	9	CL891439	CL891439 abg08h06.	c 795	20	1.0	561	6	CB072720	CB072720 taa28d10.
c 723	20	1.0	482	9	AG472666	AG472666 Mus_muscu	796	20	1.0	564	2	BF044226	BF044226 BP250002B
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c 725	20	1.0	486	6	BY596595	BY596595 BX596595	c 798	20	1.0	567	8	AZ221188	AZ221188 Sheared.D
726	20	1.0	489	2	BF769506	BF769506 RC3-IT001	c 799	20	1.0	567	8	BZ930601	BZ930601 CH240_360
727	20	1.0	490	6	CD332005	CD332005 StrPU537.	c 800	20	1.0	568	7	CF122111	CF122111 UI-HF-BP0
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c 729	20	1.0	492	6	CB083106	CB083106 hn66d10.b	c 802	20	1.0	574	9	CE298618	CE298618 tigr-g88-
730	20	1.0	493	2	BE224434	BE224434 kp62h09.y	c 803	20	1.0	576	9	CR309991	CR309991 Medicago
c 731	20	1.0	494	6	CB083022	CB083022 hn65c01.g	804	20	1.0	577	8	AZ406055	AZ406055 1M0175G11
732	20	1.0	495	1	AL801009	AL801009 AL801009	c 805	20	1.0	580	5	BF507014	BF507014 BP507014
733	20	1.0	495	8	AQ411068	AQ411068 HS_5064.B	c 806	20	1.0	580	8	AZ791848	AZ791848 2M0041J23
c 734	20	1.0	496	4	BG346851	BG346851 dad16d11.	c 807	20	1.0	581	8	BH103608	BH103608 RPCI-24-3
735	20	1.0	497	7	CG267611	CG267611 tae99c10.	c 808	20	1.0	582	7	CK958495	CK958495 4098945.B
c 736	20	1.0	498	1	AI479179	AI479179 tm55c10.x	c 809	20	1.0	582	7	CK968017	CK968017 4083156.B
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c 743	20	1.0	502	4	BG34838	BG34838 353194.MA	c 816	20	1.0	590	1	AL797531	AL797531 AL797531
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745	20	1.0	505	4	BM027094	BM027094 GIT000038	c 818	20	1.0	590	9	CE451120	CE451120 tigr-g88-
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c 747	20	1.0	505	7	CK343316	CK343316 K0940A04-	820	20	1.0	593	4	BM492005	BM492005 p9p2n.pk0
748	20	1.0	506	4	BM705670	BM705670 UI-E-DX0-	c 821	20	1.0	594	1	AL866273	AL866273 AL866273
c 749	20	1.0	508	1	AI517100	AI517100 GH27734.3	c 822	20	1.0	594	7	CK905543	CK905543 ih25d12.x
c 750	20	1.0	508	8	BH036716	BH036716 RPCI-24-3	c 823	20	1.0	595	8	AZ350172	AZ350172 1M0087B03
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753	20	1.0	512	9	CE589403	CE589403 tigr-g88-	c 826	20	1.0	598	9	CC962093	CC962093 BOIFX90TF
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C 829	20	1.0	608	9	CR833670	902	20	1.0	681	8	BH328780	BH328780	CH230-124
C 830	20	1.0	611	6	CB580485	C 903	20	1.0	682	5	BX771399	BX771399	UI-R-E10-
C 831	20	1.0	612	6	CB480349	C 904	20	1.0	682	6	CA447127	CA447127	UI-H-AE1-
C 832	20	1.0	613	5	BW365651	C 905	20	1.0	682	7	CR845142	CR845142	Medicago
C 833	20	1.0	614	1	AL797544	C 906	20	1.0	682	9	CR502176	CR502176	AA141081
C 834	20	1.0	614	4	BJ091667	C 907	20	1.0	685	1	AA141081	AA141081	CK01129.3
C 835	20	1.0	614	7	CR966903	C 908	20	1.0	687	9	AG355801	AG355801	Mus muscu
C 836	20	1.0	614	9	CL745355	C 909	20	1.0	692	8	BH949290	BH949290	od183d11.
C 837	20	1.0	615	8	BZ430345	C 910	20	1.0	695	8	AZ262461	AZ262461	RPCI-23-1
C 838	20	1.0	616	5	BQ206711	C 911	20	1.0	697	4	BM410800	BM410800	EST585127
C 839	20	1.0	616	5	BU782721	C 912	20	1.0	697	6	BZ028293	BZ028293	OGS93602.
C 840	20	1.0	616	7	CR980507	C 913	20	1.0	701	6	CA761678	CA761678	BR060012A
C 841	20	1.0	616	7	CR588487	C 914	20	1.0	701	8	BF712624	BF712624	830581 MA
C 842	20	1.0	616	9	CR833828	C 915	20	1.0	701	8	CF362790	CF362790	BOMI69TR
C 843	20	1.0	616	9	CE217647	C 916	20	1.0	703	7	CF988252	CF988252	AGENCOURT
C 844	20	1.0	617	8	BH699669	C 917	20	1.0	703	7	CR576724	CR576724	CR576724
C 845	20	1.0	617	8	CK753882	C 918	20	1.0	703	8	BH998456	BH998456	OH256d12.
C 846	20	1.0	622	7	CO209925	C 919	20	1.0	703	8	BZ481714	BZ481714	BONNB40TF
C 847	20	1.0	623	7	CK373649	C 920	20	1.0	703	9	AG516727	AG516727	Mus muscu
C 848	20	1.0	626	5	BX777758	C 921	20	1.0	704	7	CN067224	CN067224	I21_Ag2_P
C 849	20	1.0	627	8	BZ945601	C 922	20	1.0	707	5	BX770361	BX770361	BM770361
C 850	20	1.0	628	8	AZ564995	C 923	20	1.0	707	8	BZ003972	BZ003972	osm73f12.
C 851	20	1.0	630	7	CR415803	C 924	20	1.0	708	4	BM119938	BM119938	L0932G11-
C 852	20	1.0	630	8	AQ584316	C 925	20	1.0	708	4	CF175824	CF175824	799827 MA
C 853	20	1.0	632	4	BG711626	C 926	20	1.0	709	2	BS345589	BS345589	BBS34589
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C 855	20	1.0	634	6	CD450791	C 928	20	1.0	710	8	BZ260976	BZ260976	CH230-374
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C 860	20	1.0	641	4	BI113911	C 933	20	1.0	718	8	CK629199	CK629199	Mus muscu
C 861	20	1.0	641	4	BM385583	C 934	20	1.0	720	1	AJ449315	AJ449315	AG355931
C 862	20	1.0	641	9	CE528122	C 935	20	1.0	720	5	BX704206	BX704206	Forward B
C 863	20	1.0	643	4	BG711553	C 936	20	1.0	721	8	CK843162	CK843162	UI-R-Bu2-
C 864	20	1.0	643	8	AQ995413	C 937	20	1.0	721	8	BQ194634	BQ194634	UI-R-CN1-
C 865	20	1.0	644	4	BJ055200	C 938	20	1.0	722	5	BQ194634	BQ194634	UI-R-CN1-
C 866	20	1.0	644	8	BH406558	C 939	20	1.0	722	8	BS124556	BS124556	BOGLI43TR
C 867	20	1.0	644	9	AG120072	C 940	20	1.0	722	8	CR441022	CR441022	CR441022
C 868	20	1.0	646	9	BX218216	C 941	20	1.0	723	9	CL512761	CL512761	SAIL_866
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C 870	20	1.0	649	2	BH590438	C 943	20	1.0	724	5	BX504425	BX504425	8au26c12.
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C 875	20	1.0	655	1	AL853701	C 948	20	1.0	729	8	BH658246	BH658246	BOMIL33TR
C 876	20	1.0	655	9	CG942594	C 949	20	1.0	729	9	AG358931	AG358931	Mus muscu
C 877	20	1.0	655	9	CG942594	C 950	20	1.0	731	9	CR054658	CR054658	Forward B
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C 881	20	1.0	659	9	CR346516	C 954	20	1.0	736	5	CO556727	CO556727	AGENCOURT
C 882	20	1.0	660	6	CB680119	C 955	20	1.0	738	8	AQ956567	AQ956567	LEF74C06.
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C 885	20	1.0	661	5	CE772978	C 958	20	1.0	743	5	BP731370	BP731370	BP731370
C 886	20	1.0	662	5	BQ224081	C 959	20	1.0	743	8	BH691702	BH691702	BOHWT1TR
C 887	20	1.0	663	7	CO083128	C 960	20	1.0	744	9	CR148154	CR148154	Forward B
C 888	20	1.0	664	8	BH987748	C 961	20	1.0	744	9	CL096966	CL096966	ISB1-29B2
C 889	20	1.0	665	9	CL332927	C 962	20	1.0	745	6	CA464725	CA464725	AGENCOURT
C 890	20	1.0	666	4	BG478099	C 963	20	1.0	745	6	CB942485	CB942485	AGENCOURT
C 891	20	1.0	666	8	BZ522003	C 964	20	1.0	745	9	CL6113974	CL6113974	OR_BBA000
C 892	20	1.0	666	9	CE247436	C 965	20	1.0	746	8	AQ313807	AQ313807	RPCI111-94
C 893	20	1.0	666	9	CE454006	C 966	20	1.0	746	8	BU120103	BU120103	603142345
C 894	20	1.0	669	9	AG049122	C 967	20	1.0	748	4	BG786069	BG786069	SEAMC006
C 895	20	1.0	670	8	AZ263616	C 968	20	1.0	752	9	CL865567	CL865567	t4903be.f
C 896	20	1.0	675	7	CK833299	C 969	20	1.0	753	8	AQ858300	AQ858300	nbb0012K
C 897	20	1.0	679	8	AQ641944	C 970	20	1.0	753	8	BH435311	BH435311	BOGOT70TR
C 898	20	1.0	680	8	BH953535	C 971	20	1.0	753	9	CG257171	CG257171	OGFES2TH
C 899	20	1.0	680	9	AG290384	C 972	20	1.0	753	9	CG353925	CG353925	OGFA162TH
C 900	20	1.0	681	2	AW668077	C 973	20	1.0	754	7	CO045126	CO045126	UI-M-GV0-

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c 977      20      1.0      757      5      BH239301      BH239301      ATYCI23TF
c 978      20      1.0      760      6      CB595511      CB595511      AGENCOURT
c 979      20      1.0      760      6      CT734960      CT734960      OGLAR55TV
c 980      20      1.0      761      5      BU278802      BU278802      603864118
c 981      20      1.0      761      5      BU300818      BU300818      603609194
c 982      20      1.0      762      9      CL724848      CL724848      OR_BBA005
c 983      20      1.0      763      7      CR566567      CR566567      CR566567
c 984      20      1.0      764      9      AG607379      AG607379      Mus muscu
c 985      20      1.0      765      9      AG536282      AG536282      Mus muscu
c 986      20      1.0      766      9      CG023063      CG023063      ZMBBC055
c 987      20      1.0      768      5      BU222878      BU222878      603947704
c 988      20      1.0      768      5      BU361683      BU361683      603784680
c 989      20      1.0      768      8      BH247726      BH247726      BOGAV42TF
c 990      20      1.0      769      1      AU003144      AU003144      AU003144
c 991      20      1.0      770      8      BH660017      BH660017      BOHSM12TR
c 992      20      1.0      771      5      BU435916      BU435916      603256958
c 993      20      1.0      771      7      CV266016      CV266016      WS02028.B
c 994      20      1.0      773      8      BZ062799      BZ062799      11f46f11..
c 995      20      1.0      774      4      BG936566      BG936566      SS1-0945
c 996      20      1.0      774      7      CO045108      CO045108      UT-M-GVO-
c 997      20      1.0      776      8      AZ667747      AZ667747      ENTFA51TF
c 998      20      1.0      778      8      BH238347      BH238347      ATYCF80TR
c 999      20      1.0      779      4      BI968157      BI968157      GM830004B
1000      20      1.0      781      4      BI891625      BI891625      ZF637-3-0
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ALIGNMENTS

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LOCUS      SALK_092802.55.75.x Arabidopsis thaliana TDNA insertion lines
DEFINITION      Arabidopsis thaliana genomic clone SALK_092802.55.75.x, genomic
survey sequence.
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CC796106
CC796106.1      GI:32391329
GSS.
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Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 426)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednisi,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At4g20250.
Class: TDNA tagged.
Location/Qualifiers
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/clone="SALK_092802.55.75.x"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
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elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

ORIGIN
Query Match      21.0%; Score 426; DB 9; Length 426;
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Matches 426; Conservative 0; Mismatches 0;

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DB      426      TAAATTATCTATTTTATCAAAAGTTTGGTTTTAGGAAAAATGATCTTTTCATATAAAAA 367
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QY      213      ATATATAGATCTTCAAGAAACTGAAATGGGTTTTCAACTATTTTATCGTTTGACACTAC 272
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DB      366      ATATATAGATCTTCAAGAAACTGAAATGGGTTTTCAACTATTTTATCGTTTGACACTAC 307
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QY      273      TTTGACTTATCAAAAGAGTTTCAAAATAGAAAAATAGAAATCGAATCACACGTTTCAGTGT 332
      |||||
DB      306      TTTGACTTATCAAAAGAGTTTCAAAATAGAAAAATAGAAATCGAATCACACGTTTCAGTGT 247
      |||||

QY      333      AAGAGGGATTTGATATTTGTCGACATTTTAAAGAGTTTGGTTTGTGTTTTCCTCAATCTG 392
      |||||
DB      246      AAGAGGGATTTGATATTTGTCGACATTTTAAAGAGTTTGGTTTGTGTTTTCCTCAATCTG 187
      |||||

QY      393      CATGTTTTTTCGTTCCGTTGAACCAAAATCAACACTTTGTATATAACCGAATAGTAATA 452
      |||||
DB      186      CATGTTTTTTCGTTCCGTTGAACCAAAATCAACACTTTGTATATAACCGAATAGTAATA 127
      |||||

QY      453      CTAGACGTACGCCAATACCAAAAATAAAAATCAAACTCAATTCACAAATTTGAATCTACAC 512
      |||||
DB      126      CTAGACGTACGCCAATACCAAAAATAAAAATCAAACTCAATTCACAAATTTGAATCTACAC 67
      |||||

QY      513      CATATCATGCATATATATATATATATATATATATATATATATATATATATATATATAT 572
      |||||
DB      66      CATATCATGCATATATATATATATATATATATATATATATATATATATATATATATAT 7
      |||||

QY      573      AATATC 578
      |||||
DB      6      AATATC 1

RESULT 2
AQ961292/c
LOCUS      LERFK31TF LERA Arabidopsis thaliana genomic clone LERFK31, genomic
DEFINITION      survey sequence.
ACCESSION      AQ961292
VERSION      AQ961292.1      GI:6788993
KEYWORDS      GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 679)
Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T.,
Felclum,T., Liang,F., Creasy,T. and Fraser,C.M.
Genomic survey sequencing of Landsberg erecta ecotype of
Arabidopsis thaliana and identification of sequence-based
polymorphisms
Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: atcigr.org
For additional information, see http://www.tigr.org/tldb/at/at.html
Seq primer: TF
Class: shotgun.
Location/Qualifiers

FEATURES
```



```
RESULT 4
BZ597205
LOCUS
DEFINITION
  BZ597205          412 bp      DNA      linear      GSS 07-JAN-2003
  SALK_100410.46.60.n Arabidopsis thaliana T-DNA insertion lines
  Arabidopsis thaliana genomic clone SALK_100410.46.60.n, genomic
  survey sequence.
ACCESSION
  BZ597205
VERSION
  BZ597205.1      GI:27538158
KEYWORDS
  GSS.
SOURCE
  Arabidopsis thaliana (thale cress)
ORGANISM
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
  1 (bases 1 to 412)
  Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R.,
  Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
  Shinn,P., Zimmerman,J. and Ecker,J.R.
  A Sequence-Indexed Library of Insertion Mutations in the
  Arabidopsis Genome
  Unpublished (2001)
  Contact: Joseph R. Ecker
  Salk Institute Genomic Analysis Laboratory (SIGNAL)
  The Salk Institute for Biological Studies
  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
  Tel: 858 453 4100 x1752
  Fax: 858 558 6379
  Email: ecker@salk.edu
  This is single pass sequence recovered from the left border of
  T-DNA.
  Class: T-DNA tagged.
  Location/Qualifiers
    1..412
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /ecotype="Col-0"
    /db_xref="taxon:3702"
    /clone="SALK_100410.46.60.n"
    /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
    /note="PCR was performed on Arabidopsis thaliana lines
    each of which contains one or more T-DNA insertion
    elements. The resultant fragment for each line was
    directly sequenced to determine the genomic sequence at
    the site of insertion. Details of the protocols used can
    be found at http://signal.salk.edu/tdna\_protocols.html"
ORIGIN
  Query Match          12.7%; Score 258; DB 8; Length 412;
  Best Local Similarity 100.0%; Pred. No. 6.8e-110; Indels 0; Gaps 0;
  Matches 258; Conservative 0; Mismatches 0;
  QY 1353 TTCAATGTAATGAACCTGCTGTTTATTACTACTAGGCTTGTCAATATTTTCCGAGAAAT 1412
  Db 32 TTCAATGTAATGAACCTGCTGTTTATTACTACTAGGCTTGTCAATATTTTCCGAGAAAT 91
  QY 1413 ACCAGAGGAACAAAGTAGTGATTTATTCATGCAGAGTATGAAGTAATATATATACATAA 1472
  Db 92 ACCAGAGGAACAAAGTAGTGATTTATTCATGCAGAGTATGAAGTAATATATATACATAA 151
  QY 1473 ATCATGTTTGTCTCAAGCATCTAGCTGAAATATATATAAGAGTGTTCGTTGTTGA 1532
  Db 152 ATCATGTTTGTCTCAAGCATCTAGCTGAAATATATATAAGAGTGTTCGTTGTTGA 211
  QY 1533 AAAAAATATGTATGAGAAGTTTCATCTTTTCATAATAGTGAACAACTCTCTTCATACCAA 1592
  Db 212 AAAAAATATGTATGAGAAGTTTCATCTTTTCATAATAGTGAACAACTCTCTTCATACCAA 271
  QY 1593 AAAAAATTTGAAAAAAA 1610
  Db 272 AAAAAAATTTGAAAAAAA 289
  RESULT 5
CL489509/c
LOCUS
DEFINITION
  CL489509          982 bp      DNA      linear      GSS 01-APR-2004
  SAIL_525_C07.v1 SAIL Collection Arabidopsis thaliana genomic clone
  SAIL_525_C07.v1, genomic survey sequence.
ACCESSION
  CL489509
VERSION
  CL489509.1      GI:45971813
KEYWORDS
  GSS.
SOURCE
  Arabidopsis thaliana (thale cress)
ORGANISM
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
  1 (bases 1 to 982)
  Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
  Dietrich,B., Ho,P., Backaden,J., Ko,C., Clarke,J.D., Cotton,D.,
  Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
  Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
  A high-throughput Arabidopsis reverse genetics system
  Plant Cell 14 (12), 2985-2994 (2002)
  22356987
  MEDLINE
  PUBMED
  COMMENT
  Contact: Sessions A
  Applied Trait Genetics
  Syngenta Biotechnology Inc.
  3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
  Email: allen.sessions@syngenta.com
  ABRC Stock Number CS822250; T-DNA left border flanking sequences of
  Syngenta Arabidopsis Insertion Library (SAIL) lines are available
  through the Arabidopsis Biological Resource Center (ABRC).
  Sequences represent a pool of amplified genomic regions and not
  single contiguous sequences.
  Class: T-DNA tagged.
  Location/Qualifiers
    1..982
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /ecotype="Columbia"
    /db_xref="taxon:3702"
    /clone="SAIL_525_C07.v1"
    /clone_lib="SAIL Collection"
    /note="T-DNA left border sequences were isolated using a
    modified TAIL-PCR strategy"
ORIGIN
  Query Match          5.8%; Score 118; DB 9; Length 982;
  Best Local Similarity 100.0%; Pred. No. 5.2e-44; Indels 0; Gaps 0;
  Matches 118; Conservative 0; Mismatches 0;
  QY 1218 ACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTTATCGTTTCAAGTAAGTCTCTTTA 1277
  Db 175 ACAGATCAAAATACGAGGAGAGATCTCTAAAGAGATTTATCGTTTCAAGTAAGTCTCTTTA 116
  QY 1278 TCAAACTCTTATATAAACAATCAAAACATGAACACGTCGTCTCGTTTCGATTTC 1335
  Db 115 TCAAACTCTTATATAAACAATCAAAACATGAACACGTCGTCTCGTTTCGATTTC 58
  RESULT 6
CR402809
LOCUS
DEFINITION
  CR402809          194 bp      DNA      linear      GSS 02-MAY-2004
  Arabidopsis thaliana T-DNA flanking sequence GK-858C06-025968,
  genomic survey sequence.
ACCESSION
  CR402809
VERSION
  CR402809.1      GI:46943537
KEYWORDS
  GSS.
SOURCE
  Arabidopsis thaliana (thale cress)
ORGANISM
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
  1
  Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weishaar,B.
  GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
```

the identification of T-DNA insertion mutants in Arabidopsis thaliana  
 Bioinformatics 19 (11), 1441-1442 (2003)  
 22755829  
 12874060  
 2  
 Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.  
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 23117147  
 14756321  
 3  
 Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weisshaar,B.  
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
 Biotechniques 35 (6), 1164-1168 (2003)  
 14682050  
 4 (bases 1 to 194)  
 Rosso,M.G., Strizhov,N., Li,Y. and Weisshaar,B.  
 Direct Submission  
 Submitted (01-MAY-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At4g20250.  
 Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

# FEATURES source

1. 194  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-858C06-025968"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Col-0"  
 /notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

## ORIGIN

Query Match 5.5%; Score 112; DB 9; Length 194;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-41;  
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 784 ATATTTCCCACTGTGATTGATGTGACTGCGAGTGGCATATTTCCCTCCTGATTACG 843  
 Db 83 ATATTTCCCACTGTGATTGATGTGACTGCGAGTGGCATATTTCCCTCCTGATTACG 142  
 Qy 844 TTTTACCTTCTCTCTCTGTTTCCACCGTTAAATTTACTATTGTA 895  
 Db 143 TTTTACCTTCTCTCTCTGTTTCCACCGTTAAATTTACTATTGTA 194

RESULT 7  
 BH809771 246 bp DNA linear GSS 02-MAY-2002  
 LOCUS  
 DEFINITION  
 SALK\_005656 Arabidopsis thaliana T-DNA insertion lines Arabidopsis thaliana genomic clone SALK\_005656, genomic survey sequence.  
 BH809771  
 ACCSSION  
 BH809771.1 GI:20387588  
 VERSION  
 KEYWORDS  
 SOURCE  
 Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.  
 1 (bases 1 to 246)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu

## REFERENCE COMMENT

This is single pass sequence recovered from the left border of T-DNA. This sequence lies within an annotated exon of At4g20250.  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1. 246  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_005656"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more T-DNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## FEATURES source

1. 246  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_005656"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more T-DNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 5.1%; Score 103; DB 8; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-37;  
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 903 CTTTCACCTTTTAAAGAAACCCACCGAATCATACTACCGAATCATGTCT 962  
 Db 49 CTTTCACCTTTTAAAGAAACCCACCGAATCATACTACCGAATCATGTCT 108  
 Qy 963 TCATGTGACGTACAGACTTATTTCCGTTGAATTTGGTT 1005  
 Db 109 TCATGTGACGTACAGACTTATTTCCGTTGAATTTGGTT 151

## RESULT 8

CC796100/c 396 bp DNA linear GSS 01-JUL-2003  
 LOCUS  
 DEFINITION  
 SALK\_092760.46.60.n Arabidopsis thaliana T-DNA insertion lines Arabidopsis thaliana genomic clone SALK\_092760.46.60.n, genomic survey sequence.

## ACCESSION VERSION KEYWORDS SOURCE

CC796100 1 GI:32391323  
 GSS.  
 Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.  
 1 (bases 1 to 396)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

## REFERENCE AUTHORS

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGNAL)



The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379

Email: eckersalk.edu

This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within an annotated intron of At4g20250.

Class: TDNA tagged.

Location/Qualifiers

1. .396

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/ecotype="Col-0"

/db\_xref="taxon:3702"

/clone="SAUK\_092760.46.60.n"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

# ORIGIN

Query Match 4.7%; Score 95; DB 9; Length 396;  
Best Local Similarity 100.0%; Pred. No. 3.6e-33; Indels 0; Gaps 0;  
Matches 95; Conservative 0; Mismatches 0;

QY 381 TTTTCCAACTCTGCATGGTTTTCGTTCCGTTGAAACCAATTCACACITTTGTATAAACGG 440  
Db 162 TTTTCCAACTCTGCATGGTTTTCGTTCCGTTGAAACCAATTCACACITTTGTATAAACGG 103

QY 441 AATAGTATATATCTAGACGTAGCCCAATACCAAAA 475  
Db 102 AATAGTATATATCTAGACGTAGCCCAATACCAAAA 68

# RESULT 9

AV832342  
LOCUS 207 bp mRNA linear EST 01-APR-2002  
DEFINITION RAFL11 Arabidopsis thaliana cDNA clone RAFL11-12-C05 5',  
mRNA sequence.

ACCESSION AV832342

VERSION AV832342.1 GI:19874402

SOURCE EST.

ORGANISM Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 207)

Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,

Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,

Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.

and Shinozaki, K.

Large scale analysis of Arabidopsis full-length cDNA (2002b)

Unpublished (2002)

Contact: Motoaki Seki

Plant Functional Genomics Research Group

RIKEN Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359

Fax: 81-298-36-9060

Email: msekirc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially

as reported previously (Seki et al., 1998). cDNA cleaved with BamHI

and XhoI was ligated to modified lambda FLC-1 vector (Carninci et

al., submitted for publication) digested with BamHI and SalI. This

clone is in a modified pluscript vector. Please visit our web

site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further

details.

# FEATURES

source

Location/Qualifiers

1. .207

/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/db\_xref="taxon:3702"  
/clone="RAFL11-12-C05"  
/dev\_stage="plants at various developmental stages from  
germination to mature seeds"  
/lab\_host="DH10B"  
/clone\_lib="RAFL11"  
/note="Site 1: BamHI; Site 2: SalI; subjected to various  
treatments (dehydration, cold, high salt, ABA, heat and  
UV). Dark-grown plants"

# ORIGIN

Query Match 4.3%; Score 88; DB 1; Length 207;  
Best Local Similarity 100.0%; Pred. No. 7.2e-30; Indels 0; Gaps 0;  
Matches 88; Conservative 0; Mismatches 0;

QY 1177 GAGACAATTAATCAGTTTCGTTGTTGGAGAAGAAGAACAGATCAATATCAGGAG 1236  
Db 2 GAGACAATTAATCAGTTTCGTTGTTGGAGAAGAAGAACAGATCAATATCAGGAG 61

QY 1237 AGATCTCTAAAGAGATTATCGTTTCAA 1264  
Db 62 AGATCTCTAAAGAGATTATCGTTTCAA 89

# RESULT 10

AJ609323  
LOCUS 278 bp mRNA linear EST 09-JAN-2004  
DEFINITION Arabidopsis thaliana aerial vegetative tissues 4-weeks old  
Arabidopsis thaliana cDNA clone al89D6 5', mRNA sequence.

ACCESSION AJ609323

VERSION AJ609323.1 GI:40787565

KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 278)

Clepet, C., Le Clainche, I. and Caboche, M.

Improved full-length cDNA production based on RNA tagging by T4 DNA

ligase

Nucleic Acids Res. 32 (1), E6 (2004)

Contact: Clepet CY

URGV, CNRS / INRA

2 Rue Gaston-Cremlieux, 91057 Evry, France.

Location/Qualifiers

1. .278

source

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/db\_xref="taxon:3702"

/clone="al89D6"

/tissue\_type="aerial vegetative tissues"

/dev\_stage="4-weeks old"

/clone\_lib="Arabidopsis thaliana aerial vegetative tissues

4-weeks old"

/note="ecotype: Columbia 0 ; country: France"

# ORIGIN

Query Match 4.3%; Score 88; DB 1; Length 278;  
Best Local Similarity 100.0%; Pred. No. 7.1e-30; Indels 0; Gaps 0;  
Matches 88; Conservative 0; Mismatches 0;

QY 1177 GAGACAATTAATCAGTTTCGTTGTTGGAGAAGAAGAACAGATCAATATCAGGAG 1236  
Db 1 GAGACAATTAATCAGTTTCGTTGTTGGAGAAGAAGAACAGATCAATATCAGGAG 60

QY 1237 AGATCTCTAAAGAGATTATCGTTTCAA 1264  
Db 61 AGATCTCTAAAGAGATTATCGTTTCAA 88

```

RESULT 11
AV825689      507 bp  mRNA  linear  EST 01-APR-2002
LOCUS        RAFL7 Arabidopsis thaliana cDNA clone RAFL07-12-M18 5',
DEFINITION   mRNA sequence.
ACCESSION    AV825689
VERSION      AV825689.1 GI:19867749
KEYWORDS     EST
SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE    1 (bases 1 to 507)
AUTHORS      Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
              Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
              Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
              and Shinozaki,K.
              Large scale analysis of Arabidopsis full-length cDNA (2002b)
              Unpublished (2002)
              Contact: Motoaki Seki
              Plant Functional Genomics Research Group
              RIKEN Genomic Sciences Center
              3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
              Tel: 81-298-36-4359
              Fax: 81-298-36-9060
              Email: mseki@rtc.riken.go.jp
              An Arabidopsis full-length cDNA library was constructed essentially
              as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
              and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
              al., submitted for publication) digested with BamHI and SalI. This
              clone is in a modified pluscript vector. Please visit our web
              site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
              details.
FEATURES     source
              Location/Qualifiers
                1..507
                /organism="Arabidopsis thaliana"
                /mol_type="mRNA"
                /db_xref="taxon:3702"
                /clone="RAFL07-12-M18"
                /dev_stage="rosette plants"
                /lab_host="DH10B"
                /clone_lib="RAFL7"
                /note="Site 1: BamHI; Site 2: SalI; subjected to
                cold-treated (1, 2, 5, 10, 24 hr)"
ORIGIN
Query Match 4.3%; Score 88; DB 1; Length 507;
Best Local Similarity 100.0%; Pred. No. 7e-30;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1177 GAGACAAATTAATCAGTTTCGTGTTGGAGAGAGAGACAGATCAATACGAGGAG 1236
Db 3 GAGACAAATTAATCAGTTTCGTGTTGGAGAGAGAGACAGATCAATACGAGGAG 62
QY 1237 AGATCTCTAAGAGATTATCGTTTCAA 1264
Db 63 AGATCTCTAAGAGATTATCGTTTCAA 90
RESULT 12
BP562932/c    605 bp  mRNA  linear  EST 20-JUN-2004
LOCUS        BP562932 RAFL16 Arabidopsis thaliana cDNA clone RAFL16-39-009 5',
DEFINITION   mRNA sequence.
ACCESSION    BP562932
VERSION      BP562932.1 GI:48978698
KEYWORDS     EST
SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana
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              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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REFERENCE    1 (bases 1 to 605)
AUTHORS      Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
              Nakajima,M., Enju,A., Akiyama,K., Oono,Y., Muramatsu,M.,
              Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
              Arakawa,T., Shibata,K., Shinagawa,A., and Shinozaki,K.
              Functional annotation of a full-length Arabidopsis cDNA collection
              Science 296 (5565), 141-145 (2002)
              21932900
              MEDLINE
              PUBMED
              11910074
              Contact: Motoaki Seki
              Plant Functional Genomics Research Group
              RIKEN Genomic Sciences Center
              3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
              Tel: 81-298-36-4359
              Fax: 81-298-36-9060
              Email: mseki@rtc.riken.go.jp
              Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for
              further details.
FEATURES     source
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Best Local Similarity 100.0%; Pred. No. 6e-29;
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QY 1179 GACAAATTAATCAGTTTCGTGTTGGAGAGAGAGACAGATCAATACGAGGAG 1238
Db 395 GACAAATTAATCAGTTTCGTGTTGGAGAGAGAGACAGATCAATACGAGGAG 336
QY 1239 ATCTCTAAGAGATTATCGTTTCAA 1264
Db 335 ATCTCTAAGAGATTATCGTTTCAA 310
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DEFINITION   6402 Lambda-PRL2 Arabidopsis thaliana cDNA clone 115M24T7, mRNA
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              T43139
              VERSION
              T43139.1 GI:25977703
              EST
              Arabidopsis thaliana (thale cress)
              ORGANISM
              Arabidopsis thaliana
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
              1 (bases 1 to 463)
              Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
              McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M.,
              Retzel,E. and Somerville,C.
              Genes Galore: a summary of methods for accessing results from
              large-scale partial sequencing of anonymous Arabidopsis cDNA clones
              Plant Physiol. 106, 1241-1255 (1994)
              95148729
              MEDLINE
              PUBMED
              7846151
              On Nov 6, 1997 this sequence version replaced gi:933425.
              Contact: Thomas Newman
              MSU-DOE Plant Research Laboratory
              Michigan State University
              MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
              Lansing, MI
              Tel: 517-353-0854
              Fax: 517-353-9168
              Email: 22313tcn@ibm.ci.msu.edu

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FEATURES
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        quantities of 4 pools of mRNA. The mRNA sources were 1) 7
        day germinated etiolated seedlings; 2) tissue culture
        grown roots; 3) staged plants half with 24 hour light
        cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
        same plants as 3 but aerial tissue (stems, flowers and
        siliques). The vector is BRL's lambda Zip-Lox. The cDNA
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QY 1181 CAATTAATCAGTTTCGTGTTGGAGAGAAGAACAGATCAATAACGAGGAGAGAT 1240
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QY 1241 CTCTAAGAGATTTATCGTTTCAA 1264
Db      61 CTCTAAGAGATTTATCGTTTCAA 84

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DEFINITION
ACCESSION T43150
VERSION   T43150
KEYWORDS  EST.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 495)
AUTHORS   Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M.,
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
95148729
PUBMED    7846151
COMMENT    Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, Mi
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@bm.cl.msu.edu
Seq primer: T7 dye primer.
On Apr 14, 1993 this sequence version replaced gi:635738.
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, Mi
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@bm.cl.msu.edu
Seq primer: T7 dye primer.
FEATURES
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day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques). The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA. "
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RESULT 15
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DEFINITION
ACCESSION H36351
VERSION   H36351
KEYWORDS  EST.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 516)
AUTHORS   Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M.,
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
95148729
PUBMED    7846151
COMMENT    Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, Mi
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@bm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
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    quantities of 4 pools of mRNA. The mRNA sources were 1) 7
    day germinated etiolated seedlings; 2) tissue culture
    grown roots; 3) staged plants half with 24 hour light
    cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
    same plants as 3 but aerial tissue (stems, flowers and
    siliques). The vector is BRL's lambda Zip-Lox. The cDNA
    inserts were directionally cloned with Sal-Not arms using
    oligo dT primed cDNA. "
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inserts were directionally cloned with Sal-Not arms using  
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DB 1 AATTAAATCAGTTTCGTGTTTGGAGAGAGAGAACAGATCAATACGAGGAGATC 60  
QY 1242 TCTAAAGAGATTTATCGTTTCAA 1264  
DB 61 TCTAAAGAGATTTATCGTTTCAA 83

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